

Query Match 100.0%; Score 20; DB 10; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1569 AGGACTCTGAGGCTCTTTCT 1588

RESULT 2

US-09-800-909-1
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,909
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,862
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472
US-09-800-909-1

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGACTCTGAGGCTCTTTCT 20
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Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 3

US-09-800-908-2
; Sequence 2, Application US/09800908
; Patent No. US20020111462A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,908
FILING DATE: 08-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,347
FILING DATE: <Unknown>
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993

ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248635
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472
US-09-800-908-2

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 4

US-09-954-456-1187
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul

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? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00665
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00668
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00663
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00662
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00661
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: PCT/US01/00670
? PRIOR FILING DATE: 2001-01-30
? PRIOR APPLICATION NUMBER: US 60/234,687
? PRIOR FILING DATE: 2000-09-21
? PRIOR APPLICATION NUMBER: US 09/608,408
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: US 09/774,203
? PRIOR FILING DATE: 2001-01-29
? NUMBER OF SEQ ID NOS: 49117
? SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
? SEQ ID NO 423
? LENGTH: 480
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: MAP TO AP000046.1
? OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
? OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.4
? OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
? OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
? OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.5
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
? OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
US-09-864-761-423

Query Match      84.0%; Score 16.8; DB 10; Length 480;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0

Qy      1 AGGACTCTGAGGCTCTTCT 20
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Db      46 AGAGCTCTGAAGCTCTTCT 27

RESULT 6
US-09-867-701-6135
? Sequence 6135, Application US/09867701
? Patent No. US20020132237A1
? GENERAL INFORMATION:
? APPLICANT: Aglate, Paul A.
? APPLICANT: Jones, Robert
? APPLICANT: Harlocker, Susan L.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
? FILE REFERENCE: 210121.497
? CURRENT APPLICATION NUMBER: US/09/867,701
? CURRENT FILING DATE: 2001-05-29
? NUMBER OF SEQ ID NOS: 10912
? SOFTWARE: FastSeq for Windows version 4.0
? SEQ ID NO 6135
? LENGTH: 580
? TYPE: DNA
? ORGANISM: Homo sapien
US-09-867-701-6135

Query Match      84.0%; Score 16.8; DB 10; Length 580;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0

```

Oy 1 AGGACTCTGAGGCTCTTTCT 20
||||| ||||| |||||
Db 551 AGGACTATGAGGCACTTTCT 570

RESULT 7

US-09-864-761-17222/c
; Sequence 17222, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-03-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17222
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000046.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4

; OTHER INFORMATION: EST_HUMAN HIT: BF331621.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT_HIT: g111526208, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P18583, EVALUE 3.00e-30
US-09-864-761-17222

Query Match 84.0%; Score 16.8; DB 10; Length 966;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AGGACTCTGAGGCTCTTTCT 20
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Db 153 AAGACTCTGAAGCTCTTTCT 134

RESULT 8

US-09-864-761-17120/c
; Sequence 17120, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17120
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000190.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.3

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; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.1
; OTHER INFORMATION: NT HIT: g111526208, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1801337.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P18583, EVALUE 1.00e-42
US-09-864-761-17120
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Query Match      84.0%; Score 16.8; DB 10; Length 1086;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 AGGACTCTGAGGCTCTTTCT 20
   | ||||| ||||| |||||
Db 273 AAGACTCTGAAGCTCTTTCT 254
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RESULT 9

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US-09-864-761-17617/c
; Sequence 17617, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17617
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000114.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.4
; OTHER INFORMATION: EST_HUMAN HIT: A1801337.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: g111526208, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P18583, EVALUE 1.00e-42
US-09-864-761-17617
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Query Match      94.0%; Score 16.8; DB 10; Length 1086;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 AGGACTCTGAGGCTCTTTCT 20
   | ||||| ||||| |||||
Db 273 AAGACTCTGAAGCTCTTTCT 254
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RESULT 10

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US-09-864-761-12705/c
; Sequence 12705, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 12705
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC026236.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.47
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.44
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.47
US-09-864-761-12705

Query Match 80.0%; Score 16; DB 10; Length 526;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCT 16
|||||
DB 434 AGGACTCTGAGGCTCT 419

RESULT 11

US-09-729-835-13/c
; Sequence 13, Application US/09729835
; Patent No. US20010016647A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: P2015P1
; CURRENT APPLICATION NUMBER: US/09/729,835
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/257,179
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/056,270
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,271
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,247
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,073
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (766)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-729-835-13

Query Match 80.0%; Score 16; DB 10; Length 1336;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTCT 20
|||||
DB 232 AGGAYTTCAGGCTGTCTCT 213

RESULT 12
US-10-002-344A-72
; Sequence 72, Application US/10002344A
; Patent No. US20020172959A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
; FILE REFERENCE: DEX-0241
; CURRENT APPLICATION NUMBER: US/10/002,344A
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/242,998
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-002-344A-72

Query Match 79.0%; Score 15.8; DB 9; Length 239;
Best Local Similarity 89.5%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTC 19
|||||
DB 219 AGGACTCTGAGGACTTTC 237

RESULT 13

US-10-002-344A-73
; Sequence 73, Application US/10002344A
; Patent No. US20020172959A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
; FILE REFERENCE: DEX-0241
; CURRENT APPLICATION NUMBER: US/10/002,344A
; CURRENT FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/242,998
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-002-344A-73

Query Match 79.0%; Score 15.8; DB 9; Length 333;
Best Local Similarity 89.5%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTC 19
|||||
DB 220 AGGACTCTGAGGACTTTC 238

RESULT 14

US-09-867-550-1063
; Sequence 1063, Application US/09867550
; Patent No. US20020082206A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.

APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby

FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1063

LENGTH: 527
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (37)..(45)
OTHER INFORMATION: Wherein any n is one of a or t or c or g
US-09-867-550-1063

Query Match 79.0%; Score 15.8; DB 10; Length 527;
Best Local Similarity 89.5%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTC 19
Db 459 AGGTCCTCTGAGGCTCTTGC 477

RESULT 15
US-09-867-550-2118/c
Sequence 2118, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby

FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2118

LENGTH: 527
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: reverse complement of SEQ ID NO:1063
NAME/KEY: misc_feature
LOCATION: (484)..(491)
OTHER INFORMATION: Wherein any n may be a or t or g or c
US-09-867-550-2118

Query Match 79.0%; Score 15.8; DB 10; Length 527;
Best Local Similarity 89.5%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTC 19
Db 69 AGGTCCTCTGAGGCTCTTGC 51

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:30:25 : Search time 41.4471 Seconds
(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937A-5
Perfect score: 20
Sequence: 1 tcacagagagtcaggacctt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
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6: gb.pat.*
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41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	20	100.0	870	11	G15915	G15915 human STS C
C 2	20	100.0	2224	6	ARI52033	ARI52033 Sequence
C 3	20	100.0	2253	6	A78517	A78517 Sequence 1
C 4	20	100.0	2394	9	HUMTNFR11	M55994 Human tumor
C 5	20	100.0	2613	9	HSTNFR2S10	U52165 Human tumor
C 6	20	100.0	3380	11	G26865	G26865 human STS S
C 7	20	100.0	3452	9	S63368	S63368 Homo sapien
C 8	20	100.0	3633	6	AX333705	AX333705 Sequence
C 9	20	100.0	3683	6	AX348016	AX348016 Sequence
C 10	20	100.0	3683	6	AX348018	AX348018 Sequence
C 11	20	100.0	3683	6	AX348020	AX348020 Sequence
C 12	20	100.0	3683	9	HUMNFR	M32315 Human tumor
C 13	20	100.0	115602	9	HS1118D24	AL031276 Human DNA
C 14	20	100.0	122105	2	AL355998	AL355998 Homo sapi
C 15	20	100.0	187877	2	AC023251	AC023251 Homo sapi
C 16	19	95.0	21	12	AB068557	AB068557 Synthetic
C 17	19	95.0	212467	2	AL691472	AL691472 Mus muscu
C 18	19	95.0	213281	2	AL683882	AL683882 Mus muscu
C 19	18.4	92.0	2339	6	A26415	A26415 cDNA fragme
C 20	18.4	92.0	136652	2	AC125086	AC125086 Mus muscu
C 21	18.4	92.0	209877	9	AC012509	AC012509 Homo sapi
C 22	18.4	92.0	333300	2	AC125091	AC125091 Mus muscu
C 23	18	90.0	1124	9	HSCOA8	AJ001544 Homo sapi
C 24	17.4	87.0	92558	9	HS341E18	AL031178 Human DNA
C 25	17.4	87.0	110000	2	LMFLCHR31_01	Continuation (2 of
C 26	17.4	87.0	130338	2	AC104844	AC104844 Oryza sat
C 27	17.4	87.0	139594	2	AC025085	AC025085 Homo sapi
C 28	17.4	87.0	151040	2	AC020827	AC020827 Mus muscu
C 29	17.4	87.0	153926	9	AL160059	AL160059 Human DNA
C 30	17.4	87.0	154109	2	AC108965	AC108965 Rattus no
C 31	17.4	87.0	159384	2	AL356110	AL356110 Homo sapi
C 32	17.4	87.0	160359	2	AC119584	AC119584 Rattus no
C 33	17.4	87.0	166801	2	AC103240	AC103240 Rattus no
C 34	17.4	87.0	169668	2	AL845322	AL845322 Danio rer
C 35	17.4	87.0	172042	2	AC108305	AC108305 Rattus no
C 36	17.4	87.0	185896	2	AC059564	AC059564 Mus muscu
C 37	17.4	87.0	188867	2	AC129341	AC129341 Rattus no
C 38	17.4	87.0	201188	10	AC124169	AC124169 Mus muscu
C 39	17.4	87.0	205883	2	AC102603	AC102603 Mus muscu
C 40	17.4	87.0	221975	2	AC124710	AC124710 Mus muscu
C 41	17.4	87.0	267278	2	AC122252	AC122252 Mus muscu
C 42	17	85.0	20	12	AB068555	AB068555 Synthetic
C 43	17	85.0	2365	9	AK092743	AK092743 Homo sapi
C 44	17	85.0	69631	2	AC126386	AC126386 Homo sapi
C 45	17	85.0	93821	2	AC021596	AC021596 Homo sapi

ALIGNMENTS

RESULT 1
G15915/c

LOCUS human STS CHLC UTR_02819_M32315.870 bp DNA linear STS 19-JAN-1996
DEFINITION sequence tagged site.

ACCESSION G15915.1
VERSION G15915.1 GI:1161804
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens vector=pjCpl host=E.coli dut+ung+ (DH10B) Marker
Selected genomic DNA prepared from XY individual of French
nationality.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)

AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K. H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: UTR_02819_M32315, CHLC_UTR_02819_M32315.T36190
 Contact: Dr. Jeffrey C. Murray

UofI
 The University of Iowa
 Department of Pediatrics, Iowa City, IA 52242, USA
 Tel: (319) 356-3508
 Fax: (319) 356-3347
 Email: jeff-murray@iowa.edu

Primer A: CCTGTGACTCTCTGTGACCTG
 Primer B: GTCTTCATGGTCACTCAGG
 STS size: 206
 PCR Profile:

denature: 30 seconds at 94 degrees C
 annealing: 75 seconds at 55 degrees C
 extension: 15 seconds at 72 degrees C
 PCR cycles: 27
 extension: 6 minutes at 72 degrees C

Protocol:
 Template: 30ng genomic DNA
 Primer: each 1.5 pmole
 dNTPs: each 200 uM
 Tag Polymerase: 0.3 units
 Total Vol: 10 uL

Buffer:
 MgCl2: 1.5mM
 KCl: 50mM
 Tris: 10mM
 pH: 8.3

Prepared with primer pairs derived from M32315.

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
 /db_xref="taxon:9606"

272..477

272..291

complement(458..477)

157 a 246 c 279 g 188 t

BASE COUNT

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 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
 Db 287 TCACAGAGAGTCAGGGACTT 268

RESULT 2

AR152033/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

AR152033
 Sequence 2 from patent US 6232446.
 AR152033
 AR152033.1 GI:15118083

Unknown.
 Unknown.
 Unclassified.
 1 (bases 1 to 2224)
 Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
 TNF ligands
 Patent: US 6232446-A 2 15-MAY-2001;
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/organism="unknown"

435 a 698 c 689 g 402 t

Query Match 100.0%; Score 20; DB 6; Length 2224;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
 Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 3

A78517/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

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/organism="unidentified"

/db_xref="taxon:32644"

90..1475

/note="unnamed protein product"

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/db_xref="GI:6090180"

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 DOVETQACTREONRICTCRPGWYCALSKQEGCLCAPLRCRPGFVARPGTETSDV
 CKPCAGCTESNTSSDTCRPHOICNVVAIPGNASKDAVCTSTSPTRSMAPGAVHL
 PVSTRSQHQTPTPESTAPSTFLLPMGSPPAEGSTGDFALPGLIVGTALGLLI
 GVVNCVIMTVQVKKPLCLQREAKVPHLPADKARGTQGPQQHLLITAFSSSSSS
 ASALDRRAPTRNPOAPGASGAGEARASTGSDSPFGHGTQVNVTCIVNVCSDD
 HSSQSSQASSTMGDTSDSPSPSKDEQVPFSEKCAFRSQLETPTLLGSTEEKPLP
 LGVPOAGMKPS"

BASE COUNT

ORIGIN

440 a 709 c 698 g 406 t

Query Match 100.0%; Score 20; DB 6; Length 2253;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
 Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 4

HUMTNFR1I/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.
 M55994.1 GI:339757
 glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.
 Homo histiocytic lymphoma cell line U937, cDNA to mRNA.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 2394)
 Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
 A second tumor necrosis factor receptor gene product can shed a

HUMTNFR1I
 Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.
 M55994.1 GI:339757
 glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.
 Homo histiocytic lymphoma cell line U937, cDNA to mRNA.
 Homo sapiens
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 Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
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 M55994.1 GI:339757
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 Homo histiocytic lymphoma cell line U937, cDNA to mRNA.
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 Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
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 A second tumor necrosis factor receptor gene product can shed a

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 1 (bases 1 to 2394)
 Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
 A second tumor necrosis factor receptor gene product can shed a

Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.
 M55994.1 GI:339757
 glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.
 Homo histiocytic lymphoma cell line U937, cDNA to mRNA.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 2394)
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 A second tumor necrosis factor receptor gene product can shed a

Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.
 M55994.1 GI:339757
 glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.
 Homo histiocytic lymphoma cell line U937, cDNA to mRNA.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 2394)
 Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
 A second tumor necrosis factor receptor gene product can shed a

Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.
 M55994.1 GI:339757
 glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 2394)
 Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
 A second tumor necrosis factor receptor gene product can shed a

JOURNAL naturally occurring tumor necrosis factor inhibitor
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)
PUBMED 91045991
FEATURES 2172983

source

Location/Qualifiers
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/cell_line="U937"
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93. .1478
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/codon_start=1
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/product="tumor necrosis factor receptor"
/protein_id="AAA36755.1"
/db_xref="GI:339758"

gene

CDS

1. .2394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/cell_type="histiocytic lymphoma"
1. .2394
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93. .1478
/gene="TNFR2"
/note="603. 611 and 669. 677 glycosylation site; 861. 947 transmembrane domain; 948. 1478 cytoplasmic domain; 159. 860 extracellular domain"
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/db_xref="GI:339758"

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PVSTRSQHTPTPEPTAPSTFLPMGPSPPAEGSTGDFALPGLVIGVATGLLII
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159. .1475
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ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2394;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGTCAGGACTT 20

Db 1765 TCACAGAGTCAGGACTT 1746

RESULT 5
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LOCUS Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 10 and
DEFINITION complete cds.
VERSION U52165
KEYWORDS U52165.1 GI:1469539
SEGMENT 10 of 10
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2613)
Beltzinger, C.P., White, P.S., Maris, J.M., Sulman, E.P., Jensen, S.J.,
Lepaslier, D., Stallard, B.J., Goeddel, D.V., de Sauvage, F.J. and
Brodeur, G.M.
Physical mapping and genomic structure of the human TNFR2 gene
Genomics 35 (1), 94-100 (1996)
8661109
PUBMED

REFERENCE 2 (bases 1 to 2613)
Beltzinger, C.P., White, P.S., Maris, J.M., Sulman, E.P., Jensen, S.J.,
Lepaslier, D., Stallard, B.J., Goeddel, D.V., de Sauvage, F.J. and
Brodeur, G.M.
Physical mapping and genomic structure of the human TNFR2 gene
Genomics 35 (1), 94-100 (1996)
8661109
PUBMED

REFERENCE 2 (bases 1 to 2613)
Beltzinger, C.P., White, P.S., Maris, J.M., Sulman, E.P., Jensen, S.J.,

Lepaslier, D., Stallard, B.J., Goeddel, D.V., de Sauvage, F.J. and
Brodeur, G.M.
Direct Submission
Submitted (25-MAR-1996) Christian P. Beltzinger, Division of
Oncology, ARC Rm. 902 D, Children's Hospital of Philadelphia, 324
South 34th Street, Philadelphia, PA 19104-4318, USA
Location/Qualifiers
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/chromosome="1"
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U52159.1:1. .136,U52160.1:1. .100,U52161.1:1.95. .330,
U52162.1:1.83. .160,U52163.1:1.7. .41,U52164.1:1.7. .211,125. .2613)
/product="tumor necrosis factor receptor"
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U52159.1:1.7. .136,U52160.1:1.7. .100,U52161.1:1.95. .330,
U52162.1:1.83. .160,U52163.1:1.7. .41,U52164.1:1.7. .211,125. .405)
/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAC50622.1"
/db_xref="GI:1469541"

source

mRNA

CDS

gene

Intron

exon

BASE COUNT 553 a 750 c 742 g 568 t

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2613;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCACAGAGTCAGGACTT 20

Db 692 TCACAGAGTCAGGACTT 673

RESULT 6

G26865/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3380)

Myers, R.M.

Unpublished (1995)

COMMENT

CONTACT: Richard M. Myers

Stanford Human Genome Center (SHGC)

Stanford University School of Medicine

Department of Genetics, M-344, Stanford, CA 94305, USA

G26865 human STS SHGC-31494, sequence tagged site.
G26865 G26865.1 GI:1375115
STS; STS sequence; primer; sequence tagged site.
Homo sapiens.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3380)

Myers, R.M.

Unpublished (1995)

CONTACT: Richard M. Myers

Stanford Human Genome Center (SHGC)

Stanford University School of Medicine

Department of Genetics, M-344, Stanford, CA 94305, USA

Tel: 4157259687
Fax: 4157259689
Email: myers@shc.stanford.edu

Primer A: CCCACACTAGGACTCTGA
Primer B: CACAGAGACTCAGGACTTGC
STS size: 201
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from M23215
-- Washington University/Merck EST sequence.

FEATURES

source

1. .3380
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="1"

STS

primer_bind 1561..1761
primer_bind 1561..1580
complement(1741..1761)
BASE COUNT 703 a 1029 c 1004 g 644 t

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 3380;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGACTCAGGACTT 20

|||||
Db 1762 TCACAGAGACTCAGGACTT 1743

RESULT 7

S63368/c

LOCUS S63368 3492 bp mRNA linear PRI 06-MAR-2001
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, partial cds.
ACCESSION S63368
VERSION S63368.1 GI:235648

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 3492)

Dembic, Z., Loetscher, H., Gubler, U., Pan, Y. C., Lahm, H. W., Gentz, R.,

Brockhaus, M. and Lesslauer, W.

Two human TNF receptors have similar extracellular, but distinct

intracellular, domain sequences

Cytokine 2 (4), 231-237 (1990)

91370690

1966549

PUBMED

GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 63368] from the original journal article.

This sequence comes from Figure 1.

Location/Qualifiers

FEATURES

source

1. .3492

/organism="Homo sapiens"

/db_xref="taxon:9606"

<1..1278

/note="75-kda; This sequence comes from Figure 1; TNF

receptor"

/codon_start=1

/product="tumor necrosis factor receptor"

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/db_xref="GI:13236879"

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STYTOLMMNVPECLSGSRCSDDVQCTQACTREONRICTCRPGHYCALSKOEGRLCA

PLURKCRPGVAPRGCTETSDVCKPCACPTESNTTSTDICRPHQICNVVATPGNASM

DAVCTSTPTSRKAPGAVHLPOPVSTRSQHTQPTPEPTAPSTFLLPMGSPPAEGS

TGDFALPGLIVGTALGLIIGVNVCKKRLPQNPQAPGVASGAGARASTGSSDS

SPGQHLITAPSSSSSSLESSALDRRAPTRNQPQAPGVASGAGARASTGSSDS

SPGQHTQNVNVTCTVNVGSSSSSSQSSQASSTNGTDSSTSPSPKDEQVPFSPKEEC

AFRSQLETPTLLGSTEKPLPLGVDPDAGMKPS"

BASE COUNT 757 a 1031 c 1006 g 698 t

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 3492;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGACTCAGGACTT 20

|||||

Db 1565 TCACAGAGACTCAGGACTT 1546

RESULT 8

AX333705/c

LOCUS AX333705 3683 bp DNA linear PAT 09-JAN-2002

DEFINITION Sequence 4214 from Patent WO0194629.

ACCESSION AX333705

VERSION AX333705.1 GI:18124424

KEYWORDS human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.

1

Young, P. E., Augustus, M., Carter, K. C., Ebner, R. R., Endress, G.,

Horrikan, S., Soppet, D. R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

gene sets

Patent: WO 0194629-A 4214 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers

1. .3683

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 781 a 1098 c 1086 g 718 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;

Best Local Similarity 100.0%; Pred. No. 1.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGACTCAGGACTT 20

|||||

Db 1762 TCACAGAGACTCAGGACTT 1743

RESULT 9

AX348016/c

LOCUS AX348016 3683 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 49 from Patent EP1172444.

ACCESSION AX348016

VERSION AX348016.1 GI:18614126

KEYWORDS human.

SOURCE Homo sapiens

Location/Qualifiers

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber,S., Hampe,J. and Mascheretti,S.
Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
Patent: EP 1172444-A 49 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
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90..1475
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CKPCAPGTFSTNTSSDIDICRPHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
PVSTRSQHTOPTPEPSTAPSTFLLPMGPPPAEGSTGDFALPVLGVLTALGLLII
GVVNCVIMTVQVKKKPLCLQREAKVPHLPADKARGTGQPEQOHLITAPSSSSSSLESS
ASALDRRAPTRNOPQAPGVEASGAGEARASTGSSDPGGHGTQVNVTCIVNVCSSSD
HSSQCSQASSTMGDTSDSPSPKDEQVFPFKECAFRSQLETPTETLLGSTEEKPLP
LGVPDAGMKPS"
156
mat_peptide 781 a 1098 c 1086 g 718 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
|||||
Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 10
AX348018/c
LOCUS
DEFINITION
Sequence 51 from Patent EP1172444.
ACCESSION
AX348018
VERSION
AX348018.1 GI:18614128
KEYWORDS
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber,S., Hampe,J. and Mascheretti,S.
Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
Patent: EP 1172444-A 51 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
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LGVPDAGMKPS"
156
mat_peptide 781 a 1098 c 1086 g 718 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
|||||
Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 10
AX348018/c
LOCUS
DEFINITION
Sequence 51 from Patent EP1172444.
ACCESSION
AX348018
VERSION
AX348018.1 GI:18614128
KEYWORDS
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber,S., Hampe,J. and Mascheretti,S.
Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
Patent: EP 1172444-A 51 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
1..3683
/organism="Homo sapiens"
/db_xref="taxon:9606"
90..1475
/feature="unnamed protein product"
/codon_start=1
/protein_id="CAD22796.1"
/db_xref="GI:18614129"
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LGVPDAGMKPS"
156
mat_peptide 781 a 1098 c 1086 g 718 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
|||||
Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 12
HUMAN/c
LOCUS
DEFINITION
Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION
M32315
VERSION
M32315.1 GI:189185
KEYWORDS
c-myc proto-oncogene; necrosis factor receptor.
SOURCE
Homo sapiens lung cDNA to mRNA.
```

```

ASALDRRAPTRNOPQAPGVEASGAGEARASTGSSDPGGHGTQVNVTCIVNVCSSSD
HSSQCSQASSTMGDTSDSPSPKDEQVFPFKECAFRSQLETPTETLLGSTEEKPLP
LGVPDAGMKPS"
156
mat_peptide 780 a 1098 c 1087 g 718 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
|||||
Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 11
AX348020/c
LOCUS
DEFINITION
Sequence 53 from Patent EP1172444.
ACCESSION
AX348020
VERSION
AX348020.1 GI:18614130
KEYWORDS
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Schreiber,S., Hampe,J. and Mascheretti,S.
Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
Patent: EP 1172444-A 53 16-JAN-2002;
Conaris Research Institute GmbH (DE)
Location/Qualifiers
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/db_xref="taxon:9606"
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CKPCAPGTFSTNTSSDIDICRPHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQ
PVSTRSQHTOPTPEPSTAPSTFLLPMGPPPAEGSTGDFALPVLGVLTALGLLII
GVVNCVIMTVQVKKKPLCLQREAKVPHLPADKARGTGQPEQOHLITAPSSSSSSLESS
ASALDRRAPTRNOPQAPGVEASGAGEARASTGSSDPGGHGTQVNVTCIVNVCSSSD
HSSQCSQASSTMGDTSDSPSPKDEQVFPFKECAFRSQLETPTETLLGSTEEKPLP
LGVPDAGMKPS"
156
mat_peptide 780 a 1098 c 1088 g 717 t
BASE COUNT
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGTCAGGACTT 20
|||||
Db 1762 TCACAGAGTCAGGACTT 1743

RESULT 12
HUMAN/c
LOCUS
DEFINITION
Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION
M32315
VERSION
M32315.1 GI:189185
KEYWORDS
c-myc proto-oncogene; necrosis factor receptor.
SOURCE
Homo sapiens lung cDNA to mRNA.
```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3683)
AUTHORS Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P.,
Jerzy,R., Dower,S.K., Cosman,D. and Goodwin,R.G.
TITLE A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins
JOURNAL Science 248 (4958), 1019-1023 (1990)
MEDLINE 90260639
PUBMED 2160731
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by C.A.Smith, 30-MAR-1990, for release after publication.
FEATURES
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1..3683
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1..3683
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90..1475
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KVPSRQHTQPTPSTPSFLLPMGPSPPAEGSTGDFALPVLGIVGTALGLLII
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LGVPDAGMKPS"
90..155
/gene="tnfr"
156..1472
/gene="tnfr"
/product="tumor necrosis factor receptor"
BASE COUNT 781 a 1098 c 1086 g 718 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 3683;
Best local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCACAGAGACTCAGGACTT 20
|||||
Db 1762 TCACAGAGACTCAGGACTT 1743
RESULT 13
LOCUS HS1118D24
DEFINITION Human DNA sequence from clone 1118D24 on chromosome 1p36, 11-36.33.
Contains part of a novel gene similar to worm genes T08G11.1 and
C25H3.9, part of a 60S Ribosomal Protein L10 LiKE (pseudo)gene and
two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2
(75 kd) (TNF Binding Protein 2, TBPI1, TNF-R2, CD120B, TNFR).
Contains ESTs, STSS, GSSs, genomic marker D1S434 and a ca repeat
polymorphism, complete sequence.
ACCESSION AL031276
VERSION AL031276.1 GI:3947780
KEYWORDS HTG; 60S Ribosomal Protein L10; C25H3.9; ca repeat polymorphism;
CD120B; D1S434; T08G11.1; TBPI1; TNF Binding Protein 2; TNF-R2;
TNFR; TNFR2; Tumor Necrosis Factor Receptor 2.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 115602)
AUTHORS Heath,P.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT requests: clonerequest@sanger.ac.uk
On Dec 2, 1998 this sequence version replaced gi:3724207.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 1118D24. This sequence
has been finished according to sequencing map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre Chromosome 1
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
1118D24 is from the library RPC15 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/ VECTOR: pcypac2.
FEATURES
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/db_xref="taxon:9606"
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/complement(join(<1..161,2974..3184,6887..>6907))
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/note="match: ESTs AA099549 AA099548
supported by GENSCAN"
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/db_xref="GI:4007092"
/db_xref="SPTREMBL:O95536"
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KYKLIRGLLENLGEPIEEFMRPYDLQ"
400..677
/note="AluJb repeat: matches 1..279 of consensus"
678..865
/note="94 copies 2 mer ga 64% conserved"
prim_transcript 963..1520
/note="match: ESTs AA258456 AA258386"
repeat_region 1677..1797
/note="MIR repeat: matches 51..176 of consensus"
repeat_region 1824..2133
/note="AluSg repeat: matches 5..310 of consensus"
repeat_region 2152..2413
/note="AluSc repeat: matches 46..307 of consensus"
repeat_region 2418..2569
/note="L2 repeat: matches 2578..2749 of consensus"
repeat_region 2671..2966
/note="AluX repeat: matches 1..297 of consensus"
repeat_region 3591..3823
/note="L2 repeat: matches 1985..2218 of consensus"
repeat_region 3824..4120
/note="AluSc repeat: matches 1..299 of consensus"
repeat_region 4121..4505
/note="L2 repeat: matches 2218..2731 of consensus"
repeat_region 4637..4916


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5243. .5384
/note="MIR repeat: matches 2. .155 of consensus"
repeat_region 5385. .5643
/note="AluY repeat: matches 54. .311 of consensus"
repeat_region 5644. .5726
/note="MIR repeat: matches 155. .234 of consensus"
repeat_region 6026. .6347
/note="AluX repeat: matches 1. .307 of consensus"
prim_transcript 8059. .8580
/note="match: EST AA489193"
repeat_region 9367. .9716
/note="MER7A repeat: matches 1. .346 of consensus"
repeat_region 9717. .10429
/note="MER21B repeat: matches 39. .792 of consensus"
repeat_region 10473. .10537
/note="MIR repeat: matches 197. .262 of consensus"
repeat_region 10870. .11006
/note="MIR repeat: matches 63. .195 of consensus"
repeat_region 11007. .11107
/note="L1PA16 repeat: matches 5807. .5916 of consensus"
repeat_region 11108. .11417
/note="AluX repeat: matches 1. .310 of consensus"
repeat_region 11418. .11495
/note="L1PA16 repeat: matches 5916. .6000 of consensus"
repeat_region 11496. .11569
/note="MER21B repeat: matches 257. .335 of consensus"
repeat_region 11570. .11703
/note="L1PA16 repeat: matches 6000. .6157 of consensus"
repeat_region 12508. .12917
/note="L1M4 repeat: matches 2762. .3194 of consensus"
repeat_region 12919. .12958
/note="L1MC/D repeat: matches 2648. .2690 of consensus"
repeat_region 12959. .13253
/note="AluX repeat: matches 1. .297 of consensus"
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repeat_region 13368. .13502
/note="MIR repeat: matches 69. .200 of consensus"
repeat_region 13752. .13927
/note="L2 repeat: matches 2572. .2749 of consensus"
repeat_region 13931. .14016
/note="MIR repeat: matches 166. .253 of consensus"
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/note="L1M4 repeat: matches 4086. .4436 of consensus"
repeat_region 14786. .15134
/note="L1MC/D repeat: matches 2863. .5805 of consensus"
repeat_region 15225. .15582
/note="L1ME repeat: matches 5417. .5824 of consensus"
repeat_region 16370. .16674
/note="AluX repeat: matches 1. .305 of consensus"
repeat_region 16795. .17083
/note="AluSc repeat: matches 1. .289 of consensus"
repeat_region 18657. .18729
/note="MIR repeat: matches 183. .256 of consensus"
repeat_region 18823. .18676
/note="MER5B repeat: matches 1. .51 of consensus"
repeat_region 18877. .19183
/note="AluSg repeat: matches 1. .306 of consensus"
repeat_region 19184. .19297
/note="MER5B repeat: matches 51. .176 of consensus"
repeat_region 19329. .19638
/note="AluSg repeat: matches 1. .307 of consensus"
repeat_region 19836. .19930
/note="MIR repeat: matches 47. .146 of consensus"
repeat_region 19991. .20263
/note="AluJo repeat: matches 6. .284 of consensus"
repeat_region 20878. .21173
/note="AluY repeat: matches 2. .296 of consensus"
repeat_region 21662. .21943
/note="AluJb repeat: matches 1. .300 of consensus"
repeat_region 22233. .22366
/note="FLAM_C repeat: matches 1. .130 of consensus"
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repeat_region 22474. .22774
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repeat_region 22992. .23155
/note="MER5A repeat: matches 52. .187 of consensus"
repeat_region 24136. .24225
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repeat_region 29428. .29725
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 104308 TCACAGAGTCACGGGACTT 104327

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DEFINITION Homo sapiens chromosome 1 clone RP5-1125M11, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
ACCESSION AL355998
VERSION AL355998.9 GI:15523662
KEYWORDS HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 122105)
AUTHORS Smith,M.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 7, 2001 this sequence version replaced gi:13897067.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ1125M11
```

```

----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 121044 bases at least Q40
Consensus quality: 121310 bases at least Q30
Consensus quality: 121451 bases at least Q20
Insert size: 122105; sum-of-contigs
Insert size: 142339; 6.8% error; agarose-fp
Quality coverage: 8.74x in Q20 bases; sum-of-contigs Quality
coverage: 7.58x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 114918 TCACAGAGACTCAGGACTT 114899

RESULT 15
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LOCUS
DEFINITION Homo sapiens chromosome 1 clone RP11-353D18 map 1, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
AC023251
AC023251.3 GI:8076833
KEYWORDS HTG: HTGS_PHASE1: HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
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Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
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Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,A., Travers,M., Trigilio,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo.A., Wu.X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (10-FEB-2000) Whitehead Institute/MIT Center for Genome

```

REFERENCE
AUTHORS

Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 187877)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,F.,
 Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
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 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
 Vassiliev,H., Viel,R., Vo.A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 25, 2000 this sequence version replaced gi:7139786.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WITBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L6342
 Center clone name: 353_D_18
 ----- Summary Statistics
 Sequencing vector: M13: M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 177330 bases at least Q40
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 Insert size: 188000; agarose-fp
 Insert size: 185477; sum-of-contigs
 Quality coverage: 4.9 in Q20 bases; agarose-fp
 Quality coverage: 4.9 in Q20 bases; sum-of-contigs

TITLE
JOURNAL
COMMENT

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 25 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 1587: contig of 1587 bp in length
 * 1588 1687: gap of 100 bp
 * 1688 3808: contig of 2121 bp in length
 * 3809 3908: gap of 100 bp
 * 3909 6391: contig of 2483 bp in length
 * 6392 6491: gap of 100 bp
 * 6492 8438: contig of 1947 bp in length
 * 8439 8538: gap of 100 bp
 * 8539 11095: contig of 2557 bp in length
 * 11096 11195: gap of 100 bp
 * 11196 14256: contig of 3061 bp in length
 * 14257 14356: gap of 100 bp
 * 14357 18925: contig of 4569 bp in length
 * 18926 19025: gap of 100 bp
 * 19026 22429: contig of 3404 bp in length

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* 22430 22529: gap of 100 bp
* 22530 27710: contig of 5181 bp in length
* 27711 27810: gap of 100 bp
* 27811 33955: contig of 6145 bp in length
* 33956 34055: gap of 100 bp
* 34056 39058: contig of 5003 bp in length
* 39059 39158: gap of 100 bp
* 39159 44172: contig of 5014 bp in length
* 44173 44272: gap of 100 bp
* 44273 50808: contig of 6536 bp in length
* 50809 50908: gap of 100 bp
* 50909 57062: contig of 6154 bp in length
* 57063 57162: gap of 100 bp
* 57163 64064: contig of 6902 bp in length
* 64065 64164: gap of 100 bp
* 64165 70384: contig of 6220 bp in length
* 70385 70484: gap of 100 bp
* 70485 77931: contig of 7447 bp in length
* 77932 78031: gap of 100 bp
* 78032 85239: contig of 7208 bp in length
* 85240 85339: gap of 100 bp
* 85340 93719: contig of 8380 bp in length
* 93720 93819: gap of 100 bp
* 93820 102274: contig of 8455 bp in length
* 102275 102374: gap of 100 bp
* 102375 113890: contig of 11516 bp in length
* 113891 113990: gap of 100 bp
* 113991 124382: contig of 10392 bp in length
* 124383 124482: gap of 100 bp
* 124483 138011: contig of 13529 bp in length
* 138012 138111: gap of 100 bp
* 138112 154313: contig of 16202 bp in length
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Query Match 100.0%; Score 20; DB 2; Length 187877;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGACTCAGGACTT 20
 |||
 Db 144611 TCACAGAGAGTCAGGACTT 144592

Search completed: December 6, 2002, 03:57:24
 Job time : 170.647 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 4.80891 Seconds
(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937A-5

Perfect score: 20

Sequence: 1 tcacagagagtcaggagactt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002:*

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- 23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAA49211	Human tumour necro
C 2	20	100.0	2224	AAQ89544	p75 Tumour Necrosi
C 3	20	100.0	2393	AAQ10907	40kD TNF inhibitor
C 4	20	100.0	2394	AAQ83951	Human 40 kDa TNF i
C 5	20	100.0	2613	AAA49207	Human tumour necro
C 6	20	100.0	3683	ABK83997	Human cDNA differe
C 7	20	100.0	3683	ABL65877	Lung cancer relate
C 8	20	100.0	3683	ABK33465	Human TNF receptor
C 9	20	100.0	3683	ABK33466	Human TNF receptor

C 10	20	100.0	3683	24	ABK33467	Human TNF receptor
C 11	19	95.0	21	24	ABL43100	Human chromosome 1
C 12	19	95.0	201	19	AAQ12093	Human biallelic po
C 13	18.4	92.0	2339	12	AAQ10956	Encodes human 75kd
C 14	18.4	92.0	2339	20	AAQ09171	Human tumour necro
C 15	18.4	92.0	2339	22	AAH48860	Human TNFBP-associ
C 16	16.8	84.0	22870	22	AAS41989	Genomic sequence #
C 17	16.8	84.0	22870	22	AAS42010	Genomic sequence #
C 18	16.8	84.0	22870	22	AAK80760	Human immune/haema
C 19	16.8	84.0	22870	22	AAK87148	Human immune/haema
C 20	16.8	84.0	23432	22	AAS35832	Human cDNA differe
C 21	16.8	84.0	220895	24	ABK84798	Human cardiovascu
C 22	16.4	82.0	316	24	ABN76219	Human ORFX polyu
C 23	16.4	82.0	1699	21	AAC69613	Human secreted pro
C 24	16.4	82.0	167343	24	ABL64403	Stomach cancer rel
C 25	16.4	82.0	167343	24	ABL67239	Thyroid cancer rel
C 26	16	80.0	2779	23	ABL24698	Drosophila melanog
C 27	16	80.0	5136	22	AAH44289	Human spliced tran
C 28	15.8	79.0	60	24	ABN40943	Human secreted pro
C 29	15.8	79.0	285	21	AAC18156	Hepatitis C virus
C 30	15.8	79.0	340	17	AAT27971	Human polynucleoti
C 31	15.8	79.0	344	22	AAI88677	Human nervous syst
C 32	15.8	79.0	546	22	ABA20255	Arabidopsis thalia
C 33	15.8	79.0	1039	21	AAC47150	Human secreted pro
C 34	15.8	79.0	3301	19	AAV34209	Genomic sequence #
C 35	15.8	79.0	6019	23	ABK42832	Barley Mla6-A geno
C 36	15.8	79.0	6793	23	ABL50539	Genomic sequence #
C 37	15.8	79.0	7153	23	ABL50540	Barley Mla6-A geno
C 38	15.8	79.0	9581	22	AAS28461	Genomic sequence #
C 39	15.8	79.0	11234	22	ABA20857	Human nervous syst
C 40	15.8	79.0	107820	22	AAI16230	Human ATP-binding
C 41	15.8	79.0	140036	24	AAS98600	Human genomic DNA
C 42	15.4	77.0	35	21	AA559431	Primer for DNA enc
C 43	15.4	77.0	340	17	AAT27973	Hepatitis C virus
C 44	15.4	77.0	383	21	AAC26586	Human secreted pro
C 45	15.4	77.0	475	21	AAC79720	Human secreted pro

ALIGNMENTS

RESULT 1

AAA49211

ID AAA49211 standard; DNA; 20 BP.

XX AAA49211;

XX 22-NOV-2000 (first entry)

DT Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-8.

DE Human tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;

XX Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;

KW osteoporosis; PCR primer; ss.

XX Homo sapiens.

XX WO200032826-A1.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US28403.

XX 30-NOV-1998; 98US-0110268.

XX (UYDR-) UNIV DREXEL.

XX Spotila LD;

XX WPI; 2000-412362/35.

XX Identifying individuals at risk of developing osteoporosis comprises

PT assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene

PT in a DNA sample from an individual .

SQ Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other;
 Query Match 100.0%; Score 20; DB 16; Length 2224;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCACAGAGAGTCAGGGACTT 20
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 DB 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 3
 ID AAQ10907/c
 XX AAQ10907 standard; cDNA; 2393 BP.
 AC AAQ10907;
 XX
 DT 13-MAY-1991 (first entry)
 XX
 DE 40kD TNF inhibitor precursor gene in c40DK#6.
 XX
 KW Tumour necrosis factor; inhibitor; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 93..1478
 FT /*tag= a
 PN AU9058976-A.
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 PD 24-JAN-1991.
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 PF 16-JUL-1990; 90AU-0058976.
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 PR 07-FEB-1990; 90US-0479661.
 PR 18-JUL-1989; 89US-0381080.
 PR 11-DEC-1989; 89US-0450329.
 XX
 PA (SYNE-) SYNERGEN INC.
 XX
 DR WPI; 1991-073847/11.
 DR P-PSDB; AAR11001.
 XX
 PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha
 PT and -beta, useful as therapeutic agent.
 XX
 PS Disclosure; Fig 39; 142pp; English.
 CC
 CC The sequence encodes the entire 40 kD TNF inhibitor. The clone from
 CC which the sequence was obt'd. was isolated from a cDNA library
 CC prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
 CC gene can be inserted into expression vectors for prep'n. of TNF
 CC inhibitor for use in the treatment of inflammatory and degenerative
 CC diseases.
 CC See also AAQ10878, AAQ10884 and AAQ10883.
 XX
 SQ Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;

Query Match 100.0%; Score 20; DB 12; Length 2393;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCACAGAGAGTCAGGGACTT 20
 |||||
 DB 1764 TCACAGAGAGTCAGGGACTT 1745

RESULT 4
 AAC83951/c
 ID AAC83951 standard; DNA; 2394 BP.
 XX
 AC AAC83951;

XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Human 40 kDa TNF inhibitor precursor coding sequence.
 XX
 KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
 KW 1L-1; inflammatory disease; degenerative disease; human; lymphotoxin; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6143866-A.
 XX
 PD 07-NOV-2000.
 XX
 PF 19-JAN-1995; 95US-0375242.
 XX
 PR 19-JUL-1990; 90US-0555274.
 PR 09-JUL-1993; 93US-0090366.
 PR 18-JUL-1989; 89US-0381080.
 PR 11-DEC-1989; 89US-0450329.
 PR 07-FEB-1990; 90US-0479661.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
 PI Vanderslice RW, Vannice J, Kohno T;
 XX
 DR WPI; 2001-006443/01.
 DR P-PSDB; AAB37686.
 XX
 PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
 PT non-native cysteine residue cross-linked with polyethylene glycol,
 PT useful for treating inflammatory and degenerative diseases mediated by
 PT TNF -
 XX
 PS Example 12; Fig 39; 82pp; English.
 CC
 CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
 CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
 CC novel TNF inhibitors of the present invention are useful as therapeutic
 CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
 CC for treating inflammatory and degenerative diseases mediated by TNF. The
 CC present sequence is the coding sequence for the precursor of 40 kDa TNF
 CC inhibitor. The 40 kDa TNF inhibitor can inhibit both TNF alpha and beta
 CC (lymphotoxin).
 XX
 SQ Sequence 2394 BP; 484 A; 743 C; 738 G; 428 T; 1 other;

Query Match 100.0%; Score 20; DB 22; Length 2394;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCACAGAGAGTCAGGGACTT 20
 |||||
 DB 1765 TCACAGAGAGTCAGGGACTT 1746

RESULT 5
 AAA49207/c
 ID AAA49207 standard; DNA; 2613 BP.
 XX
 AC AAA49207;
 XX
 DT 22-NOV-2000 (first entry)
 XX
 DE Human tumour necrosis factor alpha receptor 2 gene exon 10.
 XX
 KW Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
 KW osteoporosis; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

```

FT CDS      1..2613
FT          /tag= a "TNR2"
FT          /product= "partial
FT allele    replace (593,A), (598,G), (620,T)
FT          /tag= b
FT allele    /label= allele_1
FT          replace (593,A), (598,T), (620,T)
FT          /tag= c
FT allele    /label= allele_2
FT          replace (593,G), (598,T), (620,C)
FT          /tag= d
FT allele    /label= allele_3
FT          replace (593,G), (598,T), (620,T)
FT          /tag= e
FT allele    /label= allele_4
FT          replace (593,A), (598,T), (620,C)
FT          /tag= f
FT          /label= allele_5
FT WO200032826-A1.
FT PN
FT PD
FT PD
FT XX
FT XX
FT PF      30-NOV-1999; 99WO-US28403.
FT XX
FT PR      30-NOV-1998; 98US-0110268.
FT XX
FT PA      (UYDR-) UNIV DREXEL.
FT PI
FT PI      Spotila LD;
FT XX
FT DR      WPI; 2000-412362/35.
FT XX
FT PT      Identifying individuals at risk of developing osteoporosis comprises
FT PT      assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
FT PT      in a DNA sample from an individual -
FT XX
FT PS      Claim 2: Page 17-18; 21pp; English.
FT PS
FT CC      The present sequence comprises exon 10 of the human tumour necrosis
FT CC      factor alpha receptor 2 (TNFR2) gene. The sequence contains three
FT CC      polymorphic sites. By determining the genotype of an individual it is
FT CC      possible to identify those at risk of osteoporosis, which is
FT CC      characterised by low bone density and fragile bones, later in life. Those
FT CC      at greatest risk are those who possess allele 1, which is the rarest
FT CC      allele. This is particularly useful as many cases of osteoporosis go
FT CC      undetected at present.
FT XX
FT SQ      Sequence 2613 BP: 553 A; 750 C; 742 G; 568 T; 0 other;
FT
FT Query Match      100.0%; Score 20; DB 21; Length 2613;
FT Best Local Similarity 100.0%; Pred. No. 2.6;
FT Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
QY      1 TCACAGAGCTCAGGGACTT 20
DB      692 TCACAGAGCTCAGGGACTT 673
      |||||
RESULT 6
ABK83997/c
ID ABK83997 standard; cDNA: 3683 BP.
XX
XX AC      ABK83997;
XX
XX DT      14-AUG-2002 (first entry)
XX
XX DE      Human cDNA differentially expressed in granulocytic cells #568.
XX
XX KW      Human; ss; granulocytic cell; DNA chip; bacterial infection;
XX KW      viral infection; parasitic infection; protozoal infection;
XX KW      fungal infection; sterile inflammatory disease; psoriasis;

```

```

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
XX granulocyte activation; chronic inflammation; allergy.
OS Homo sapiens.
XX
XX PN      WO200228999-A2.
XX
XX PD      11-APR-2002.
XX
XX PF      03-OCT-2001; 2001WO-US30821.
XX
XX PR      03-OCT-2000; 2000US-237189P.
XX
XX PA      (GENE-) GENE LOGIC INC.
XX
XX PI      Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
XX PT      Detecting granulocyte activation by detecting differential expression
XX PT      of genes associated with granulocyte activation, which serves as
XX PT      diagnostic markers that is useful for monitoring disease states and
XX PT      drug toxicity -
XX
XX PS      Claim 1; SEQ ID No 568; 114pp; English.
XX
XX CC      The invention relates to detecting (M1) granulocyte (GC) activation
XX CC      (GCA), by detecting the level of expression of gene(s) (Gs) identified by
XX CC      DNA chip analysis as given in the specification, and comparing
XX CC      the expression level to an expression level in an unactivated
XX CC      GC, where differential expression of Gs is indicative of GCA.
XX CC      Also included are modulating (M2) GA by contacting GC with an agent
XX CC      that alters the expression of at least one gene in Gs; (2) screening (M3)
XX CC      for an agent capable of modulating GCA or an inflammation (especially
XX CC      chronic) in a tissue, an allergic response in a subject, exposure of a
XX CC      subject to a pathogen or sterile inflammatory disease using the
XX CC      gene expression profile; (3) detecting (M4) an inflammation (especially
XX CC      chronic) in a tissue, an allergic response in a subject, exposure of a
XX CC      subject to a pathogen or sterile inflammatory disease, by detecting the
XX CC      level of expression in a sample of the tissue of gene(s) from Gs, where
XX CC      (4) treating (M5) an inflammation (especially chronic) or in a tissue,
XX CC      an allergic response in a subject, exposure of a subject to a pathogen
XX CC      or sterile inflammatory disease, by contacting a tissue having
XX CC      inflammation with an agent that modulates the expression of gene(s)
XX CC      from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
XX CC      modulating GA; M3 is useful for screening an agent capable of modulating
XX CC      GCA preferably in an inflammation in a tissue; M4 is useful for
XX CC      detecting an inflammation (especially chronic) in a tissue, an allergic
XX CC      response in a subject, exposure of a subject to a pathogen or sterile
XX CC      inflammatory disease (e.g. psoriasis, rheumatoid arthritis, renal
XX CC      glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
XX CC      reperfusion injury, ARDS, adult respiratory distress syndrome,
XX CC      inflammatory bowel disease, Crohn's disease, ulcerative colitis,
XX CC      periodontal disease; also bacterial infection, viral infection,
XX CC      parasitic infection, protozoal infection, fungal infection and M5 is
XX CC      useful for treating one of the above conditions. The present
XX CC      sequence represents a gene differentially expressed in granulocytes.
XX CC      Note: The sequence data for this patent did not form part
XX CC      of the printed specification, but was obtained in electronic
XX CC      format directly from WIPO at
XX CC      ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ      Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

```

```

Query Match      100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCACAGAGACTCAGGGACTT 20

```



```
XX PI Schreiber S, Hampe J, Mascheretti S;
XX DR WPI: 2002-156651/21.
XX DR P-PSDB; AAU75172.
XX PT Detecting non-responders to anti-human necrosis factor therapy.
XX PT comprises testing an individual for homozygosity for a single
XX PT nucleotide polymorphism in the gene coding for the tumour necrosis
XX PT factor receptor II -
XX PS Disclosure: Page 23-27; 45pp; English.
XX CC The present invention relates to a method for detecting non-responders
XX CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
XX CC an individual for homozygosity for at least one single nucleotide
XX CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
XX CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
XX CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
XX CC Met196Arg respectively, are also described. The method of the invention
XX CC is useful for detecting non-responders to anti-TNF therapy such as
XX CC infliximab therapy, or therapy of Crohn's disease. The genes containing
XX CC the 2 novel polymorphisms are useful for diagnostic purposes in
XX CC inflammatory, malignant or other chronic diseases. The present sequence
XX CC encodes for human TNF receptor II.
XX SQ Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 9
ABK33466/c
ID ABK33466 standard; DNA; 3683 BP.
XX AC ABK33466;
XX DT 23-APR-2002 (first entry)
XX DE Human TNF receptor II gene with SNP in exon 2.
XX KW Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
XX KW chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
XX KW inflammatory disorder; chronic disease; receptor; gene;
XX KW single nucleotide polymorphism; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 90..1475
XX FT /*tag= a
XX FT /product= "TNF receptor II variant #1"
XX FT 90..155
XX FT /*tag= b
XX FT sig_peptide
XX FT mat_peptide 156..1472
XX FT /*tag= c
XX FT variation replace (257, A)
XX FT /*tag= d
XX FT /standard_name= "Single nucleotide polymorphism"
XX PN EP1172444-A1.
XX PD 16-JAN-2002.
XX XX 10-JUL-2000; 2000EP-0114786.
XX PF 10-JUL-2000; 2000EP-0114786.
```

```
XX PA (CONA-) CONARIS RES INST GMBH.
XX PI Schreiber S, Hampe J, Mascheretti S;
XX DR WPI: 2002-156651/21.
XX DR P-PSDB; AAU75173.
XX PT Detecting non-responders to anti-human necrosis factor therapy,
XX PT comprises testing an individual for homozygosity for a single
XX PT nucleotide polymorphism in the gene coding for the tumour necrosis
XX PT factor receptor II -
XX PS Claim 15; Page 29-33; 45pp; English.
XX CC The present invention relates to a method for detecting non-responders
XX CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
XX CC an individual for homozygosity for at least one single nucleotide
XX CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
XX CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
XX CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
XX CC Met196Arg respectively, are also described. The method of the invention
XX CC is useful for detecting non-responders to anti-TNF therapy such as
XX CC infliximab therapy, or therapy of Crohn's disease. The genes containing
XX CC the 2 novel polymorphisms are useful for diagnostic purposes in
XX CC inflammatory, malignant or other chronic diseases. The present sequence
XX CC represents the human TNF receptor II gene containing the SNP in exon 2.
XX SQ Sequence 3683 BP; 780 A; 1098 C; 1087 G; 718 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 10
ABK33467/c
ID ABK33467 standard; DNA; 3683 BP.
XX AC ABK33467;
XX DT 23-APR-2002 (first entry)
XX DE Human TNF receptor II gene with SNP in exon 6.
XX KW Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
XX KW chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
XX KW inflammatory disorder; chronic disease; receptor; gene;
XX KW single nucleotide polymorphism; ds.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 90..1475
XX FT /*tag= a
XX FT /product= "TNF receptor II variant #2"
XX FT 90..155
XX FT /*tag= b
XX FT sig_peptide
XX FT mat_peptide 156..1472
XX FT /*tag= c
XX FT variation replace (676, T)
XX FT /*tag= d
XX PN EP1172444-A1.
XX PD 16-JAN-2002.
XX XX 10-JUL-2000; 2000EP-0114786.
```

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XX 10-JUL-2000; 2000EP-0114786.
XX (CONA-) CONARIS RES INST GMBH.
XX Schreiber S, Hampe J, Mascheretti S;
XX WPI: 2002-156651/21.
XX P-PSDB; AAU75174.
XX
XX Detecting non-responders to anti-human necrosis factor therapy,
XX comprises testing an individual for homozygosity for a single
XX nucleotide polymorphism in the gene coding for the tumour necrosis
XX factor receptor II -
XX
XX Claim 16; Page 35-39; 45pp; English.
XX
XX The present invention relates to a method for detecting non-responders
XX to anti-tumour necrosis factor (TNF) therapy. The method involves testing
XX an individual for homozygosity for at least one single nucleotide
XX polymorphism (SNP) in the gene coding for TNF receptor II, which is
XX located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
XX A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
XX Met196Arg respectively, are also described. The method of the invention
XX is useful for detecting non-responders to anti-TNF therapy such as
XX infliximab therapy, or therapy of Crohn's disease. The genes containing
XX the 2 novel polymorphisms are useful for diagnostic purposes in
XX inflammatory, malignant or other chronic diseases. The present sequence
XX represents the human TNF receptor II gene containing the SNP in exon 6.
XX
XX Sequence 3683 BP; 780 A; 1098 C; 1088 G; 717 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 24; Length 3683;
XX Best Local Similarity 100.0%; Pred. No. 2.7;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TCACAGAGAGTCAGGGACTT 20
XX ID 1762 TCACAGAGAGTCAGGGACTT 1743
XX
XX RESULT 11
XX ABL43100
XX ID ABL43100 standard; DNA; 21 BP.
XX
XX AC ABL43100;
XX
XX DT 11-APR-2002 (first entry)
XX
XX DE Human chromosome 1p36-35 PCR primer SEQ ID NO:144.
XX
XX KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
XX genome; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN JP2001321190-A.
XX
XX PD 20-NOV-2001.
XX
XX PF 12-MAR-2001; 2001JP-0068285.
XX
XX PR 10-MAR-2000; 2000JP-0066716.
XX
XX PA (RIKA) RIKAGAKU KENKYUSHO.
XX PA (GENO-) GENOTEX YG.
XX
XX DR WPI: 2002-144136/19.
XX
XX PT Arraying genome clones -
XX
XX PS Claim 4; Page 7; 528pp; Japanese.
XX

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```

CC The present invention describes a method of arraying genome clones. The
CC method comprises: (a) clones of the genomic libraries contained in
CC multiwell plates numbered for discrimination are mixed in each of the
CC multiwell plates; (b) a primer designed based on the chromosome marker
CC sequence is added to the mixture to carry out an amplification reaction;
CC (c) a signal corresponding to the marker is detected from the resultant
CC amplified product to specify the discrimination Nos. of the multiwell
CC plates containing the clones having said marker sequence; (d) the order
CC of the markers is changed so that the same discrimination Nos. succeed to
CC the maximum in the specified discrimination Nos. to array the multiwell
CC plates; (e) the clones in the multiwell plates of the specified
CC discrimination Nos. are mixed respectively in each wells of longitudinal
CC and lateral directions; (f) the mixed clones are cultured and the
CC resultant cultures are amplified by using the above primer; (g) signals
CC are detected from the amplified products; (h) the clones in the multiwell
CC plates are specified from the detected result; and (i) the clones are
CC reconstituted as the positions on the chromosome and arrayed. The
CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
CC represent PCR primers for human chromosome 21q22.1, which are
CC specifically claimed for use in the present invention.
XX
XX Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 other;
XX
XX Query Match 95.0%; Score 19; DB 24; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4.6;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 CACAGAGAGTCAGGGACTT 20
XX ID 1 CACAGAGAGTCAGGGACTT 19
XX
XX RESULT 12
XX AAX12093/c
XX ID AAX12093 standard; DNA; 201 BP.
XX
XX AC AAX12093;
XX
XX DT 30-MAR-1999 (first entry)
XX
XX DE Human biallelic polymorphic DNA fragment M32315b.
XX
XX KW Polymorphism: biallelic; human; forensic; paternity testing; disease;
XX detection; phenotypic typing; characteristic; infection; hereditary;
XX autoimmune disease; cancer; inflammation; drug; therapy; medication;
XX treatment; marker; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9820165-A2.
XX
XX PD 14-MAY-1998.
XX
XX PF 05-NOV-1997; 97WO-US20313.
XX
XX PR 06-NOV-1996; 96US-0030455.
XX
XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX PI Hudson T, Lander ES, Wang D;
XX
XX DR WPI: 1998-286974/25.
XX
XX PT New isolated nucleic acid segments from the human genome - used for
XX determining polymorphic forms for use in e.g. forensics, paternity
XX testing or phenotypic typing for disease
XX
XX PS Claim 1; Page 219; 310pp; English.
XX
XX CC AAX10269-X12937 are human DNA fragments which contain biallelic
XX polymorphic markers which have been isolated using the primers
XX represented in AAX09121-X10268. The base occupying the polymorphic site

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CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
 CC can be used in methods for determining polymorphic forms in an individual
 CC for use in e.g. forensics, paternity testing or for phenotypic typing for
 CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan
 CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
 CC familial hypercholesterolemia, polycystic kidney disease, hereditary
 CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
 CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
 CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
 CC autoimmune diseases, inflammation, cancer, diseases of the nervous
 CC system, infection by pathogenic microorganisms, and characteristics such
 CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
 CC endurance, fertility, and susceptibility or receptivity to particular
 CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
 CC segments can also be used to produce medicaments for the treatment or
 CC prophylaxis of such diseases.

XX
 SQ Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

Query Match 95.0%; Score 19; DB 19; Length 201;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CACAGACAGTCAGGGACTT 20
 Db 201 CACAGACAGTCAGGGACTT 183
 |||||

RESULT 13
 AAQ10956/c
 ID AAQ10956 standard; DNA; 2339 BP.

XX AC AAQ10956;

XX DT 24-MAY-1991 (first entry)

XX DE Encodes human 75kD TNF-binding protein.

XX KW Tumour Necrosis Factor; binding proteins; septic shock;
 KW autoImmune glomerulonephritis; lymphokine; cytokine.

XX FH Key Location/Qualifiers
 FT CDS 1..1179
 FT /*tag= a
 FT /product= 75kD TNF-BP

XX EP417563-A.

XX PN 20-MAR-1991.

XX PD 31-AUG-1990; 90EP-0116707.

XX PF 20-APR-1990; 90CH-0001347.

XX PR 12-SEP-1989; 89CH-0003319.

XX PA (HOFF) HOFFMANN-LA ROCHE AG.

XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaeger EJ;

XX DR WPI; 1991-081851/12.

XX P-PSDB; AAR11605.

XX PT Insoluble tumour necrosis factor binding proteins - and DNA
 PT encoding them, useful in pharmaceutical prods. and for antibody
 PT prodn.

XX PS Claim 4; Fig 1; 26pp; German.

XX Partial amino acid sequences were determined for the 55 and 75kD
 CC TNF-BPs (see AAR1072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used

CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gtl1. Positive clones were
 CC identified and sequenced. Repeated sequencing showed a discrepancy
 CC at position 7 such that the third codon encodes either Thr or Ser.
 CC DNA constructs comprising the TNF-BP coding sequence may also
 CC contain a fragment encoding a human Ig domain. Recombinant
 CC constructs are used to transform cells to confer improved TNF-
 CC binding properties.
 CC See also AAQ10955.

XX SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other;

Query Match 92.0%; Score 18.4; DB 12; Length 2339;
 Best Local Similarity 95.0%; Pred. No. 16;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 TCACAGACAGTCAGGGACTT 20
 Db 1465 TCACAGACAGTCAGGGACTT 1446
 |||||

RESULT 14
 AAZ09171/c
 ID AAZ09171 standard; cDNA; 2339 BP.

XX AC AAZ09171;

XX DT 18-OCT-1999 (first entry)

XX DE Human tumour necrosis factor binding protein cDNA fragment.

XX KW Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
 KW anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
 KW autoImmune glomerulonephritis; cerebral malaria; immune response;
 KW antagonist; diagnosis; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT CDS 1..1179
 FT /*tag= a
 FT /product= "TNF binding protein"
 FT /note= "Partial sequence, no start codon given"

XX EP939121-A2.

XX PD 01-SEP-1999.

XX PF 31-AUG-1990; 90EP-0116707.

XX PR 20-APR-1990; 90CH-0001347.

XX PR 12-SEP-1989; 89CH-0003319.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
 PI Schlaeger E;

XX DR WPI; 1999-480840/41.

XX P-PSDB; AAY30935.

XX PT New insoluble proteins, and fragments, that bind to tumor necrosis
 PT factor, used to treat e.g. septic shock or cerebral malaria

XX PS Claim 4a; Fig 4; 25pp; German.

XX This invention describes novel homogeneous insoluble proteins (I),
 CC their (in)soluble fragments (Ia) and their salts that can bind tumour
 CC necrosis factor (TNF). The products of the invention have
 CC anti-inflammatory and antimalarial activity. (I) and (Ia) are used (1)
 CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
 CC glomerulonephritis, cerebral malaria, immune responses and inflammation),

CC (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
 CC diagnostic determination of TNF in body fluids. Antibodies raised against
 CC (I) are used for affinity purification of (I). This sequence encodes
 CC a tumour necrosis factor binding protein fragment described in the method
 CC of the invention.

XX
 SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;
 Query Match 92.0%; Score 18.4; DB 20; Length 2339;
 Best Local Similarity 95.0%; Pred. No. 16;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCACAGAGAGTCAGGACTT 20
 ||||| |||||
 Db 1465 TCACAGAGACTCAGGACTT 1446

RESULT 15

AAH48860/c
 ID AAH48860 standard; DNA: 2339 BP.

XX
 AC AAH48860;

XX
 DT 12-NOV-2001 (first entry)

XX
 DE Human TNFBP-associated DNA #2.

XX
 KW TNF: Lumor necrosis factor binding protein; TNFBP; treatment;
 KW insoluble protein; antinflammatory; immunosuppressive; antibacterial;
 KW antiprotocool; treatment; meningococcal sepsis; cerebral malaria;
 KW autoimmune glomerulonephritis; ds.

XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT CDS 1..1179
 FT /*tag= a
 FT /product= "TNFBP-associated protein"

XX
 PN EP1132471-A2.

XX
 PD 12-SEP-2001.

XX
 PF 31-AUG-1990; 2001EP-0108117.

XX
 PR 12-SEP-1989; 89CH-0003319.

XX
 PR 08-MAR-1990; 90CH-0000746.

XX
 PR 20-APR-1990; 90CH-0001347.

XX
 PR 31-AUG-1990; 90EP-0116707.

XX
 PR 31-AUG-1990; 99EP-0100703.

XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX
 PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
 PI Schlaeger E;

XX
 DR WPI: 2001-559312/63.

XX
 DR P-PSDB; AAB86818.

XX
 PT New homogeneous, insoluble proteins that bind tumor necrosis factor
 PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -

XX
 PS Claim 4a; Fig 4; 26pp; German.

XX
 CC This invention describes novel insoluble proteins (I), also their
 CC (in)soluble fragments and pharmaceutically acceptable salts, able to bind
 CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
 CC invention have antinflammatory, immunosuppressive, antibacterial,
 CC antiprotocool activity. (I), and related recombinant proteins, are used
 CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
 CC sepsis; development of autoimmune glomerulonephritis and cerebral
 CC malaria. Also (I), or antibodies specific for them, are used for
 CC diagnostic determination of TNF in body fluids, for affinity purification

CC of TNF and for identifying (antagonists of TNF. This sequence encodes a
 CC human TNF binding protein described in the method of the invention.

XX
 SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

Query Match 92.0%; Score 18.4; DB 22; Length 2339;
 Best Local Similarity 95.0%; Pred. No. 16;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCACAGAGAGTCAGGACTT 20
 ||||| |||||
 Db 1465 TCACAGAGACTCAGGACTT 1446

Search completed: December 5, 2002, 23:30:10
 Job time : 9.80891 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 : Search time 38.2783 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937A-5

Perfect score: 20

Sequence: 1 tcacagagagtcaggactt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rtd: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	337	10 AW801622	AW801622 IL5-UM006
C 2	20	100.0	372	9 AA031826	AA031826 zk14b11.r
C 3	20	100.0	384	9 AA353635	AA353635 EST61785
C 4	20	100.0	472	10 AV746487	AV746487 AV746487
5	20	100.0	640	10 BE299702	BE299702 600944393
C 6	20	100.0	655	14 BQ632819	BQ632819 i128d03.y

C 7	20	100.0	974	12 BG745202	BG745202 602723532
C 8	20	100.0	1053	14 BQ52282	BQ52282 AGENCOURT
C 9	20	100.0	1066	12 BF568708	BF568708 602184353
C 10	20	100.0	1102	14 BM917316	BM917316 AGENCOURT
C 11	20	100.0	1183	12 BF569011	BF569011 602184353
C 12	20	100.0	1470	12 BF569050	BF569050 602184408
C 13	20	100.0	2291	11 BC011844	BC011844 Homo 8801
C 14	18	90.0	932	12 BG829828	BG829828 602764119
C 15	17.4	87.0	121	17 BH352650	BH352650 CH230-55A
C 16	17.4	87.0	310	10 BB221242	BB221242 BB221242
C 17	17.4	87.0	450	17 AQ812560	AQ812560 HS-5249_B
C 18	17.4	87.0	623	17 AZ837703	AZ837703 2M0133B08
C 19	17	85.0	391	17 AQ437855	AQ437855 HS_5057_A
C 20	17	85.0	392	9 AI448146	AI448146 mo63d07.x
C 21	17	85.0	452	9 AI262090	AI262090 qz28b12.y
C 22	17	85.0	687	17 AZ983907	AZ983907 2M0265A16
C 23	17	85.0	770	13 BI646518	BI646518 603277607
C 24	16.8	84.0	303	17 AZ915807	AZ915807 RPCI-24-1
C 25	16.8	84.0	332	12 BF857218	BF857218 RC5-PT019
C 26	16.8	84.0	510	17 AQ825259	AQ825259 CITBI-EI-
C 27	16.8	84.0	546	17 AZ887751	AZ887751 RPCI-24-1
C 28	16.8	84.0	572	17 AQ426991	AQ426991 CITBI-EI-
C 29	16.8	84.0	621	17 DR2A23S	AL748626 Danilo ref
C 30	16.8	84.0	710	10 BB341493	BB341493 BB341493
C 31	16.8	84.0	872	14 BQ730759	BQ730759 AGENCOURT
C 32	16.4	82.0	180	13 BM482728	BM482728 535740 MA
C 33	16.4	82.0	274	10 BB475383	BB475383 BB475383
C 34	16.4	82.0	289	10 BB324937	BB324937 BB324937
C 35	16.4	82.0	308	17 AQ647902	AQ647902 RPCI93-Dp
C 36	16.4	82.0	372	14 W40081	W40081 T2594 MVAT4
C 37	16.4	82.0	377	17 AQ637005	AQ637005 RPCI-11-4
C 38	16.4	82.0	449	17 AQ043251	AQ043251 CIT-HSP-2
C 39	16.4	82.0	487	9 AI450485	AI450485 mc34d07.y
C 40	16.4	82.0	494	17 AQ538916	AQ538916 RPCI-11-3
C 41	16.4	82.0	501	17 AQ184218	AQ184218 HS_3223_A
C 42	16.4	82.0	526	17 AQ836108	AQ836108 HS_5524_A
C 43	16.4	82.0	537	17 AQ439298	AQ439298 HS_5060_B
C 44	16.4	82.0	553	10 BE234177	BE234177 140926 MA
C 45	16.4	82.0	570	17 AQ701572	AQ701572 HS_2130_A

ALIGNMENTS

RESULT 1
AW801622
LOCUS
DEFINITION IL5-UM0068-080400-056-b02 UM0068 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW801622
VERSION AW801622.1 GI:7853492
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)

REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

TITLE
JOURNAL
MEDLINE
COMMENT

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1. 372
/organism="Homo sapiens"
/db_xref="GDB:3756495"
/db_xref="taxon:9606"
/clone="IMAGE:470493"

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source

1. .384

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/db_xref="ATCC (inhost):153861"
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/dev_stage="adult"
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XhoI"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 56;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGACTT 20
|||||
DB 38 TCACAGAGAGTCAGGACTT 19

RESULT 4
AV746487/c
LOCUS      AV746487 NPC Homo sapiens cDNA clone NPCMA05 5', mRNA sequence.
DEFINITION
ACCESSION  AV746487
VERSION    AV746487.1 GI:10904335
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 472)
AUTHORS     Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N.,
Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L., Xu, S., Gu
, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Zhang, Q.,
Han, Z., Chen, Z., Hu, R., and Chen, J.
Homo sapiens NPC library cDNA clones
Unpublished (2000)
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
Location/Qualifiers
1..472
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NPCMA05"
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/tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      63 a   137 c   150 g   112 t       10 others
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Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGACTT 20
|||||
DB 177 TCACAGAGAGTCAGGACTT 158

RESULT 5
BE299702

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LOCUS      BE299702      640 bp      mRNA      linear      EST 20-JUL-2000
DEFINITION 600944393T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960374 3',
mRNA sequence.
ACCESSION  BE299702
VERSION    BE299702.1 GI:9183450
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 640)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM53 row: j column: 23
High quality sequence start: 69
High quality sequence stop: 638.
Location/Qualifiers
1..640
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2960374"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

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BASE COUNT      141 a   203 c   174 g   122 t
ORIGIN
Query Match      100.0%; Score 20; DB 10; Length 640;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGACTT 20
|||||
DB 582 TCACAGAGAGTCAGGACTT 601

RESULT 6
BO632819/c
LOCUS      BO632819 1128003.Y1 HR85 Islet Homo sapiens cDNA clone IMAGE:6031157 5',
mRNA sequence.
ACCESSION  BO632819
VERSION    BO632819.1 GI:21684337
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 655)
AUTHORS     Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
, M., Gibbons, M., McCann, R., Cole, R., Tsagarteishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium

```

JOURNAL COMMENT	Unpublished (2000) Other_ESTs: il28d03.xl Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@iobp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 484. Location/Qualifiers	source
FEATURES	1..655 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:6031157" /clone_lib="HR85 islet" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size selected on agarose gel. Average insert size -1kb. 5' xhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."	
BASE COUNT	122 a 179 c 207 g 147 t	
ORIGIN		
Query Match	100.0%; Score 20; DB 14; Length 655;	
Best Local Similarity	100.0%; Pred. No. 66;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TCACAGAGAGTCAGGGACTT 20 	
Db	80 TCACAGAGAGTCAGGGACTT 61	
RESULT 7		
BG745202/c		
LOCUS	974 bp mRNA linear EST 15-MAY-2001	
DEFINITION	602723532f1 NTH_MGC_113 Homo sapiens cDNA clone IMAGE:4850143 5', mRNA sequence.	
ACCESSION	BG745202.1 GI:14055855	
VERSION	BG745202.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 974) NTH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
COMMENT		
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BASE COUNT	216 a 328 c 297 g 212 t	
ORIGIN		
Query Match	100.0%; Score 20; DB 14; Length 1053;	
Best Local Similarity	100.0%; Pred. No. 75;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TCACAGAGAGTCAGGGACTT 20 	
Db	128 TCACAGAGAGTCAGGGACTT 109	
RESULT 8		
BQ052282		
LOCUS	1053 bp mRNA linear EST 29-MAR-2002	
DEFINITION	AGENCOURT_6868457 NTH_MGC_106 Homo sapiens cDNA clone IMAGE:5933511 5', mRNA sequence.	
ACCESSION	BQ052282	
VERSION	BQ052282.1 GI:19811622	
KEYWORDS	EST.	
SOURCE	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1053) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Daniel McVicar, DBS/NCI cDNA Library Preparation: Rubin Laboratory DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM2118 row: c column: 16 High quality sequence stop: 649. Location/Qualifiers	
FEATURES		
source		


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Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGGACTT 20
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Db 633 TCACAGAGAGTCAGGGACTT 652

RESULT 9
BF568708/c
LOCUS 1066 bp mRNA linear EST 12-DEC-2000
DEFINITION 602184353F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 5',
mRNA sequence.
ACCESSION BF568708
VERSION BF568708.1 GI:11642088
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4300500"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH_MGC Library. |"
BASE COUNT 216 a 316 c 354 g 180 t
ORIGIN
1..1066
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/notes="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: This is a NIH_MGC Library. |"

Query Match 100.0%; Score 20; DB 12; Length 1066;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGGACTT 20
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Db 671 TCACAGAGAGTCAGGGACTT 652

RESULT 10
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LOCUS 1102 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6606593 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483819
5', mRNA sequence.
ACCESSION BM917316
VERSION BM917316.1 GI:19367695
KEYWORDS EST.
SOURCE human.

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ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1102)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2012 row: b column: 12
High quality sequence stop: 507.

FEATURES

source

Location/Qualifiers
1..1102
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT

219 a 366 c 292 g 222 t 3 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 78;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGGACTT 20
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Db 284 TCACAGAGAGTCAGGGACTT 265

RESULT 11

BF569011

LOCUS

602184353T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 3',
mRNA sequence.

ACCESSION

BF569011

VERSION

BF569011.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1183)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1159 row: i column: 13
High quality sequence stop: 716.

FEATURES

source

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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(C). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
308 a 357 c 348 g 170 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 1183;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCACAGAGACTCAGGACTT 20

|||||

Db 555 TCACAGAGACTCAGGACTT 574

RESULT 12

BF569050

LOCUS

DEFINITION 602184408T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300633 3',
mRNA sequence.

ACCESSION

VERSION BF569050.1 GI:11642430

KEYWORDS

SOURCE EST.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1470)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM1159 row: 0 column: 02

High quality sequence stop: 710.

FEATURES

source

Location/Qualifiers
1. .1470
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/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(C). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

BASE COUNT

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 85;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

Db 559 TCACAGAGACTCAGGACTT 578

RESULT 13

BC011844/c

LOCUS

DEFINITION Homo sapiens, Similar to tumor necrosis factor receptor
superfamily, member 1B, clone IMAGE:4111730, mRNA.

ACCESSION

BC011844

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

1 (bases 1 to 2291)
Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK

COMMENT

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tjongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L. H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 28 Row: 1 Column: 15
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein
This clone has the following problem: incomplete processing.

FEATURES

source

Location/Qualifiers
1. .2291
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/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTB7"

BASE COUNT

ORIGIN

461 a 708 c 713 g 409 t
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Best Local Similarity 100.0%; Pred. No. 98;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 TCACAGAGACTCAGGACTT 20
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Db 1671 TCACAGAGACTCAGGACTT 1652

RESULT 14
BG829828/c
LOCUS
DEFINITION      932 bp mRNA linear EST 22-MAY-2001
                  602764119f1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4899436 5',
                  mRNA sequence.
ACCESSION      BG829828
VERSION        BG829828.1 GI:14177415
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS        1 (bases 1 to 932)
TITLE          NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL        National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT        Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: ATCC
                cDNA Library Preparation: Ling Hong/Rubin Laboratory
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone Distribution: MGC clone distribution information can be
                found through the I.M.A.G.E. Consortium/LLNL at:
                http://image.llnl.gov
                Plate: LLCM1791 row: e column: 05
                High quality sequence stop: 833.
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                /lab_host="DH10B (phage-resistant)"
                /note="organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCAGCAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by Ling
                Hong in the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library. |"
                162 a 296 c 296 g 177 t 1 others
BASE COUNT      162 a 296 c 296 g 177 t
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Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 ACAGAGACTCAGGACTT 20
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Db 782 ACAGAGACTCAGGACTT 765

RESULT 15
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LOCUS
DEFINITION      121 bp DNA linear GSS 03-DEC-2001
                  CH230-55A15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION      BH352650
VERSION        BH352650.1 GI:17283384
KEYWORDS       GSS.
SOURCE         Norway rat.
ORGANISM       Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

```

```

Rattus.
1 (bases 1 to 121)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-55A15.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 55 row: A column: 15
Seg primer: T7
Class: BAC ends.
Location/Qualifiers
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/clone="CH230-55A15"
/clone_lib="CHORI-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
BASE COUNT      32 a 30 c 29 g 30 t
ORIGIN

Query Match      87.0%; Score 17.4; DB 17; Length 121;
Best Local Similarity 94.7%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CACAGAGTCAGGACTT 20
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Db 41 CACAGAGTCAGGACTT 23

Search completed: December 6, 2002, 04:54:42
Job time : 50.2783 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 ; Search time 1.03896 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-5

Perfect score: 20

Sequence: 1 tcacagagagtcaggagctt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_NA:*
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
 - 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
 - 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
 - 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
 - 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	2224	4	US-08-477-347-2
C 2	20	100.0	2224	4	US-08-476-862-1
C 3	20	100.0	3683	4	US-09-844-634-3
C 4	20	100.0	15602	4	US-09-844-634-17
5	15.8	79.0	340	4	US-08-836-075A-69
6	15.4	77.0	35	4	US-09-502-653-51
7	15.4	77.0	340	4	US-08-836-075A-73
8	15.4	77.0	660	4	US-09-221-017B-116
9	15.4	77.0	1200	4	US-09-502-653-7
10	15.2	76.0	15936	4	US-09-147-119-1
11	14.8	74.0	199	3	US-09-058-389A-18
12	14.8	74.0	199	4	US-09-611-781-18
13	14.8	74.0	1489	4	US-09-487-445-10
14	14.8	74.0	2483	2	US-08-177-109A-1
15	14.8	74.0	2483	3	US-08-687-706-1
16	14.8	74.0	6354	3	US-09-058-389A-5
17	14.8	74.0	6354	4	US-09-611-781-5
18	14.8	74.0	45716	4	US-08-965-048-5
19	14.8	74.0	45989	4	US-08-965-048-6
20	14.4	72.0	340	3	US-08-441-971-15
21	14.4	72.0	340	4	US-08-836-075A-71
22	14.4	72.0	340	4	US-08-836-075A-77
23	14.4	72.0	340	4	US-08-836-075A-79
24	14.4	72.0	340	4	US-08-221-653-15
25	14.4	72.0	340	4	US-08-442-144A-15
26	14.4	72.0	340	4	US-08-441-970-15
C 27	14.4	72.0	492	3	US-08-600-430-1

28	14.4	72.0	523	4	US-08-896-164-13	Sequence 13, Appl
C 29	14.4	72.0	648	2	US-08-783-395-4	Sequence 4, Appl
30	14.4	72.0	1739	2	US-08-899-336-1	Sequence 1, Appl
C 31	14.4	72.0	2610	3	US-09-212-771-1	Sequence 1, Appl
C 32	14.4	72.0	2610	3	US-09-091-058-1	Sequence 1, Appl
C 33	14.4	72.0	12537	2	US-08-611-280-4	Sequence 4, Appl
C 34	14.4	72.0	12537	4	US-09-195-940-4	Sequence 4, Appl
C 35	14.4	72.0	12537	4	US-09-562-466-4	Sequence 4, Appl
36	14.2	71.0	319	1	US-08-341-568-5	Sequence 5, Appl
37	14.2	71.0	319	2	US-08-911-020-5	Sequence 5, Appl
38	14.2	71.0	485	4	US-09-085-199B-32	Sequence 32, Appl
39	14.2	71.0	571	4	US-08-991-789A-14	Sequence 14, Appl
40	14.2	71.0	571	4	US-09-062-451-14	Sequence 14, Appl
41	14.2	71.0	571	4	US-09-598-326-14	Sequence 14, Appl
42	14.2	71.0	601	4	US-09-814-951A-7	Sequence 7, Appl
43	14.2	71.0	601	4	US-09-814-951A-8	Sequence 8, Appl
44	14.2	71.0	601	4	US-09-814-951A-9	Sequence 9, Appl
45	14.2	71.0	941	2	US-08-121-436A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-477-347-2/c
; Sequence 2, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477.347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

LOCATION: 90..1472
US-08-477-347-2
Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 2
US-08-476-862-1/c
Sequence 1, Application US/08476862
Patent No. 6262239
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
TITLE OF INVENTION: ENGELMANN, Hartmut
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476.862
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989

ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25 618
REFERENCE/DOCKET NUMBER: WALLACH-12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472
US-08-476-862-1

Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 3
US-09-844-634-3/c
Sequence 3, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRE
FILE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 3

LENGTH: 3683
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)...(1475)
US-09-844-634-3

Query Match 100.0%; Score 20; DB 4; Length 3683;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 4
US-09-844-634-17/c
Sequence 17, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRE
FILE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 17

LENGTH: 15602
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 11295...11276
US-09-844-634-17

Query Match 100.0%; Score 20; DB 4; Length 15602;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 11295 TCACAGAGAGTCAGGGACTT 11276

RESULT 5
US-08-836-075A-69
Sequence 69, Application US/08836075A
Patent No. 6180768
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: STUYVER, LIEVEN

TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
US-08-836-075A-69

Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.3;

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; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-836-075A-69

Query Match 79.0%; Score 15.8; DB 4; Length 340;
Best Local Similarity 89.5%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGAGT 19
|| |||||
Db 294 TCTCAGAGAGTCAGGGAGT 312

RESULT 6
US-09-502-653-51
; Sequence 51, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schlein, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481,200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
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; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(35)
; OTHER INFORMATION: Primer: Galactanase.B.lich.upper.SacII
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-502-653-51

Query Match 77.0%; Score 15.4; DB 4; Length 35;
Best Local Similarity 94.1%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACAGAGAGTCAGGGAC 18
|||||
Db 16 CACAGAGATTCAGGGAC 32

RESULT 7
US-08-836-075A-73
; Sequence 73, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; TITLE OF INVENTION: AGENTS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-836-075A-73
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Query Match 77.0%; Score 15.4; DB 4; Length 340;
Best Local Similarity 94.1%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCACAGAGCTCAGGGA 17
Db 294 TCTCAGAGCTCAGGGA 310

RESULT 8

US-09-221-017B-116
; Sequence 116, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: ROSS, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA: PP1546
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA: PCT/AU98/01023
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141

INFORMATION FOR SEQ ID NO: 116:

SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...660

Query Match 77.0%; Score 15.4; DB 4; Length 660;
Best Local Similarity 94.1%; Pred. No. 49;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCACAGAGCTCAGGGA 17
Db 394 TCACAGAGCTCAGGGA 410

RESULT 9

US-09-502-653-7
; Sequence 7, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj invad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schleim, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481-200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Bacillus licheniformis ATCC 14580
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1197)
; OTHER INFORMATION: DNA encoding the Galactanase shown in SEQ ID NO.8.
US-09-502-653-7

Query Match 77.0%; Score 15.4; DB 4; Length 1200;
Best Local Similarity 94.1%; Pred. No. 53;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACAGAGCTCAGGAC 18
Db 4 CACAGAGCTCAGGAC 20

RESULT 10

US-09-147-119-1
; Sequence 1, Application US/09147119
; Patent No. 6338844
; GENERAL INFORMATION:
; APPLICANT: KURTH, Ruth
; APPLICANT: BAIER, Michael
; APPLICANT: BANNERT, No. 6338844bert
; APPLICANT: METZNER, Karin
; APPLICANT: WERNER, Albrecht
; TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, cDNA AND mRNA WHICH
; TITLE OF INVENTION: CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESS FOR THE
; TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/147,119
: FILING DATE: HERewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP97/01753
: FILING DATE: 10-APR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: DE 196 14 099.4
: FILING DATE: 10-APR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Wong, King L.
: REGISTRATION NUMBER: 37,500
: REFERENCE/DOCKET NUMBER: P1614-8068
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 638-5000
: TELEFAX: (202) 638-4810
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15936 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: exon
: LOCATION: 3100..3238
: FEATURE:
: NAME/KEY: exon
: LOCATION: 5540..6635
: FEATURE:
: NAME/KEY: exon
: LOCATION: 7504..7672
: FEATURE:
: NAME/KEY: exon
: LOCATION: 9711..9812
: FEATURE:
: NAME/KEY: exon
: LOCATION: 12065..12323
: FEATURE:
: NAME/KEY: exon
: LOCATION: 12578..12703
: FEATURE:
: NAME/KEY: exon
: LOCATION: 14767..15936
: US-09-147-119-1

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Query Match          76.0%; Score 15.2; DB 4; Length 15936;
Best Local Similarity 85.0%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  TCACAGAGACTCAGGGACTT 20
        ||| | ||||| |||
Db      2811 TCATAAGAGCTCAGGGTCTT 2830

RESULT 11
US-09-058-389A-18
; Sequence 18, Application US/09058389A
; Patent No. 6130065
; GENERAL INFORMATION:
; APPLICANT: Belt, Judith A.
; APPLICANT: Crawford, Charles R.
; APPLICANT: Patel, Divyen
; TITLE OF INVENTION: A TITROBENZYLMECAPTOPURINERIBOSIDE
; TITLE OF INVENTION: (NBMPR)- INSENSITIVE, EQUILIBRATIVE,
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:

```

```

1  ADDRESSEE: David A. Jackson, Esq.
2  STREET: 411 Hackensack Ave, Continental Plaza, 4th
3  STREET: Floor
4  CITY: Hackensack
5  STATE: New Jersey
6  COUNTRY: USA
7  ZIP: 07601
8  COMPUTER READABLE FORM:
9  MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: PatentIn Release #1.0, Version #1.30
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/09/058,389A
15 FILING DATE: April 9, 1998
16 CLASSIFICATION: 800
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Jackson Esq., David A.
19 REGISTRATION NUMBER: 26,742
20 REFERENCE/DOCKET NUMBER: 1340-1-013N
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 201-487-5800
23 TELEFAX: 201-343-1684
24 INFORMATION FOR SEQ ID NO: 18:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 199 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: double
29 TOPOLOGY: linear
30 MOLECULE TYPE: other nucleic acid
31 DESCRIPTION: /desc = "intron 8"
32 HYPOTHETICAL: NO
33 US-09-058-389A-18
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35 Query Match 74.0%; Score 14.8; DB 3; Length 199;
36 Best Local Similarity 88.9%; Pred. No. 83;
37 Matches 16; Conservative 0; Mismatches 2; Indels
38
39 Qy 1 TCACAGAGAGTCAGGGAC 18
40      ||||| | ||||| |||
41 Db 76 TCACAGTGGTCAGGGAC 93
42
43 RESULT 12
44 US-09-611-781-18
45 Sequence 18, Application US/09611781
46 Patent No. 6423629
47 GENERAL INFORMATION:
48 APPLICANT: Belt, Judith A.
49 APPLICANT: Crawford, Charles R.
50 APPLICANT: Patel, Diyen
51 TITLE OF INVENTION: A NITROBENZYL MERCAPTOPYRIMIDINOSIDE
52 TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEIC
53 TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME
54 NUMBER OF SEQUENCES: 22
55 CORRESPONDENCE ADDRESS:
56 ADDRESSEE: David A. Jackson, Esq.
57 STREET: 411 Hackensack Ave, Continental Plaza, 4th
58 STREET: Floor
59 CITY: Hackensack
60 STATE: New Jersey
61 COUNTRY: USA
62 ZIP: 07601
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Floppy disk
65 COMPUTER: IBM PC compatible
66 OPERATING SYSTEM: PC-DOS/MS-DOS
67 SOFTWARE: PatentIn Release #1.0, Version #1.30
68 CURRENT APPLICATION DATA:
69 APPLICATION NUMBER: US/09/611,781
70 FILING DATE:
71 CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/058,389
; FILING DATE: April 9, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-013N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "intron 8"
; HYPOTHETICAL: NO
; US-09-611-781-18

Query Match 74.0%; Score 14.8; DB 4; Length 199;
Best Local Similarity 88.9%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 TCACAGAGCTCAGGCAC 18
Db 76 TCACAGTGGCTCAGGCAC 93

RESULT 13
US-09-487-445-10
; Sequence 10, Application US/09487445
; Patent No. 6258600
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
; FILE REFERENCE: PTS-0107
; CURRENT APPLICATION NUMBER: US/09/487,445
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 10
; LENGTH: 1489
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(1489)
; US-09-487-445-10

Query Match 74.0%; Score 14.8; DB 4; Length 1489;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 ACACGAGCTCAGGCATT 20
Db 699 ACAGTGAGTCAGGCATT 716

RESULT 14
US-08-177-109A-1/c
; Sequence 1, Application US/08177109A
; Patent No. 5869615
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/058,389
; FILING DATE: April 9, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-013N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 199 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "intron 8"
; HYPOTHETICAL: NO
; US-09-611-781-18

Query Match 74.0%; Score 14.8; DB 2; Length 2483;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CACAGAGAGTCAGGCAC 19
Db 1550 CACAGAGACTCAGACT 1533

RESULT 15
US-08-687-706-1/c
; Sequence 1, Application US/08687706
; Patent No. 5928692
; GENERAL INFORMATION:
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,706
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,109
; FILING DATE: 03-JAN-1994

; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/177,109A
; FILING DATE: 03-JAN-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: WU 107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2483 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 116..2407
; OTHER INFORMATION: /note= "Product = Human Factor B"
; US-08-177-109A-1
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: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea L
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: WU 107 DIV
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 873-8794
: TELEFAX: (404) 873-8795
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2483 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo Sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 116..2407
: OTHER INFORMATION: /note= "Product = Human Factor B"
: US-08-687-706-1

Query Match 74.0%; Score 14.8; DB 2; Length 2483;
Best Local Similarity 88.9%; Pred. No 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACAGAGAGTCACGGGACT 19
Db 1550 CACAGAGACTCAGAGACT 1533
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Job time : 12.039 secs
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 20:03:23 ; Search time 0.972171 Seconds
(without alignments)
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Title: US-09-856-937A-5

Perfect score: 20

Sequence: 1 tcacagagagtcaggagctt 20

Scoring table: IDENTITY_NUC

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Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	2224	10	US-09-800-908-2 Sequence 2, Appl1
C 3	20	100.0	3683	10	US-09-954-456-1187 Sequence 1187, Ap
C 4	16.8	84.0	23432	10	US-09-764-869-1332 Sequence 1332, Ap
C 5	16.4	82.0	167343	10	US-09-962-436-281 Sequence 281, App
C 6	16.4	82.0	167343	10	US-09-964-824A-273 Sequence 273, App
C 7	15.8	79.0	3301	9	US-09-981-876-66 Sequence 66, Appl
C 8	15.8	79.0	6019	10	US-09-764-847-1719 Sequence 1719, Ap
C 9	15.8	79.0	9581	10	US-09-764-860-895 Sequence 895, App
C 10	15.4	77.0	32204	10	US-09-764-846-306 Sequence 306, App
C 11	15.2	76.0	155	10	US-09-864-761-30451 Sequence 30451, A
C 12	15.2	76.0	285	9	US-09-938-842A-2494 Sequence 2494, Ap
C 13	15.2	76.0	333	10	US-09-867-701-302 Sequence 302, App
C 14	15.2	76.0	406	10	US-09-853-386-31 Sequence 31, Appl
C 15	15.2	76.0	474	10	US-09-864-761-13882 Sequence 13882, A
C 16	15.2	76.0	792	9	US-09-736-457-220 Sequence 220, App
C 17	15.2	76.0	792	9	US-09-902-941-220 Sequence 220, App
C 18	15.2	76.0	807	9	US-09-860-670-58 Sequence 58, Appl
C 19	15.2	76.0	1077	10	US-09-770-445-130 Sequence 130, App

Sequence 3, Appl1
Sequence 1, Appl1
Sequence 15, Appl1
Sequence 607, App
Sequence 1288, Ap
Sequence 441, App
Sequence 2165, Ap
Sequence 471, App
Sequence 5, Appl1
Sequence 1445, Ap
Sequence 412, App
Sequence 414, App
Sequence 3, Appl1
Sequence 4906, Ap
Sequence 173, App
Sequence 173, App
Sequence 173, App
Sequence 1388, Ap
Sequence 1388, Ap
Sequence 3630, Ap
Sequence 28, Appl
Sequence 13, Appl
Sequence 911, App
Sequence 41, Appl

10 US-09-815-248-3
1066 10 US-09-815-248-1
400 10 US-09-732-561-15
400 10 US-09-887-576-607
446 10 US-09-917-800A-1288
758 10 US-09-822-830A-441
1859 10 US-09-880-192-33
2388 10 US-09-880-107-2165
2717 12 US-10-044-090-471
4420 9 US-09-986-234-5
8861 9 US-09-764-868-1445
8861 10 US-09-764-878-412
8887 10 US-09-764-878-414
368004 10 US-09-949-654-3
241 10 US-09-923-876-4906
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401 10 US-09-795-668-173
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402 9 US-09-948-807-1388
402 10 US-09-795-668-1388
402 10 US-09-795-686-1388
405 10 US-09-864-761-3630
500 9 US-10-060-841-28
523 10 US-09-835-992A-13
548 10 US-09-857-701-911
1830 10 US-09-771-161A-41

ALIGNMENTS

RESULT 1
US-09-800-909-1/c
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSEY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/476,862
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.

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; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-09-800-909-1

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 2
US-09-800-908-2/C
; Sequence 2, Application US/09800908
; Patent No. US2002011462A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; BELETSKY, Igor
; METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800.908
; FILING DATE: 08-Mar-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,347
; FILING DATE: <unknown>
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-09-800-908-2

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 3
US-09-954-456-1187/C
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1187
; LENGTH: 3683
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1187

Query Match 100.0%; Score 20; DB 10; Length 3683;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
Db 1762 TCACAGAGAGTCAGGGACTT 1743

RESULT 4
US-09-764-869-1332
; Sequence 1332, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17

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; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1332
; LENGTH: 23432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1332

Query Match 84.0%; Score 16.8; DB 10; Length 23432;
Best Local Similarity 90.0%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGGACTT 20
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DB 10830 TCACAGAGAGCAGGGACTT 10849

RESULT 5

US-09-962-436-281/c
; Sequence 281, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 281
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-281

Query Match 82.0%; Score 16.4; DB 10; Length 167343;
Best Local Similarity 94.4%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACAGAGAGTCAGGGACTT 20
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DB 23246 ACAGAGAGCAGGGACTT 23229

RESULT 6

US-09-964-824A-273/c
; Sequence 273, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horriagan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-964-824A-273

Query Match 82.0%; Score 16.4; DB 10; Length 167343;
Best Local Similarity 94.4%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACAGAGAGTCAGGGACTT 20
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DB 23246 ACAGAGAGCAGGGACTT 23229

RESULT 7

US-09-981-876-66
; Sequence 66, Application US/09981876
; Patent No. US20020164669A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
; CURRENT APPLICATION NUMBER: US/09/981,876
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 09/148,545
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
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; PRIOR APPLICATION NUMBER: 60/047,615
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
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; PRIOR APPLICATION NUMBER: 60/043,311
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; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 3301

Query Match 79.0%; Score 15.8; DB 9; Length 3301;
Best Local Similarity 89.5%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCACAGAGAGTCAGGACT 19

; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79
; OTHER INFORMATION: NT HIT: AL163201.2, EVALUE 2.00e-82
; OTHER INFORMATION: EST_HUMAN HIT: AAB37753.1, EVALUE 8.00e-24
; OTHER INFORMATION: SWISSPROT HIT: O77681, EVALUE 6.60e+00
US-09-864-761-30451

Query Match 76.0%; Score 15.2; DB 10; Length 155;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGACTT 20
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Db 84 TCAAAGAGAGTCAGGCGCTT 65

RESULT 12

US-09-938-842A-2494
; Sequence 2494, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2494
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2494

Query Match 76.0%; Score 15.2; DB 9; Length 285;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGACTT 20
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Db 140 TCACAGAGCGTCGCGGACTT 159

RESULT 13

US-09-867-701-302/c
; Sequence 302, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows version 4.0
; SEQ ID NO 302
; LENGTH: 333
; TYPE: DNA

; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(333)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-302

Query Match 76.0%; Score 15.2; DB 10; Length 333;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGACTT 20
||| ||||| ||||| |||
Db 173 TCACAGAGGTCAGAGCCTT 154

RESULT 14

US-09-853-386-31
; Sequence 31, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; FILE REFERENCE: P01972US1
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 406
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(406)
; OTHER INFORMATION: n equals unknown
US-09-853-386-31

Query Match 76.0%; Score 15.2; DB 10; Length 406;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCACAGAGAGTCAGGACTT 20
||| ||||| || |||||
Db 367 TCACAGAGACACAGCGGCTT 386

RESULT 15

US-09-864-761-13882/c
; Sequence 13882, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03


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; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13882
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL078471.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.79
US-09-864-761-13882

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Query Match 76.0%; Score 15.2; DB 10; Length 474;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TCACAGAGAGTCAGGGACTT 20
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Db 365 TCAAAGAGACTGAGGGCCTT 346

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Search completed: December 6, 2002, 00:19:59
Job time : 118.972 secs

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Qy	757	TTTGTGTTGTTGTTGTTGTTCTCCCTGGGCTCTG-CCCAGCTCTGGCTTCCAGAAAACC	815
Db	1830	TTTGTGTTGTTGTTGTTCTCCCTGGGCTCTGCCCAGCTCTGGCTTCCAGAAAACC	1889
Qy	816	CCAGCATCTTTCTGAGAGGGGCTTTCTGGAGAGAGGATGCTGCCTGAGTCACCCA	875
Db	1890	CCAGCATCTTTCTGAGAGGGGCTTTCTGGAGAGAGGATGCTGCCTGAGTCACCCA	1949
Qy	876	TGAAGACAGGACAGTGCCTCAGCCTCAGACTCGGGATGGTCTCTGGGGCTCTGT	935
Db	1950	TGAAGACAGGACAGTGCCTCAGCCTGAGGCTCGGGATGGTCTCTGGGGCTCTGT	2009
Qy	936	GTAGGAGGAGGTGGCAGCCCTGTAGGGAACGGGTCTTCAAAGTTAGCTCAGGAGGCTT	995
Db	2010	GCAGGAGGAGGTGGCAGCCCTGTAGGGAACGGGTCTTCAAAGTTAGCTCAGGAGGCTT	2069
Qy	996	GGAAAGCATCACCTCAGGCCAGGTGCAGTGGCTCACGCCTATGATCCCAGCACCTTGGGA	1055
Db	2070	GGAAAGCATCACCTCAGGCCAGGTGCAGTCCCTCACGCCTATGATCCCAGCACCTTGGGA	2129
Qy	1056	GGCTGAGGCGGGTGATCACCCTGAGGTTAGGAGTTCGAGACCGCTGGGCCAACATGGTA	1115
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Qy	1116	AAACCCCATCTCTACAAAAATACAGAAATTAGCCGGGCGTGGTGGCGGGCACCTATAGT	1175
Db	2190	AAACCCCATCTCTACAAAAATACAGAAATTAGCCGGGCGTGGTGGCGGGCACCTATAGT	2249
Qy	1176	CCAGCTACTCAGAAGCCTGAGGCTGGGAATCGTTTGAACCCGGGAAGCGGAGGTGCA	1235
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Qy	1236	GGGAGCGGAGATCAGCCACCTGCATCTCAGCCTGGGCGACAGCGGAGATCTGTCTCAA	1295
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AAQ10907
ID AAQ10907 standard; CDNA; 2393 BP.
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AC	AAQ10907;
XX	
XX	13-MAY-1991 (first entry)
DT	
DE	40kD TNF inhibitor precursor gene in c40DK#5.
DE	
XX	Tumour necrosis factor; inhibitor; ss.
KK	
XX	Homo sapiens.
OS	

XX (SYNE-) SYNERGEN INC.
XX PA
XX WPI; 1991-073847/11.
XX DR P-PSDB; AAR11001.
XX PT
XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha
XX and -beta, useful as therapeutic agent.
XX PS
XX Disclosure; Fig 39; 142pp; English.
XX CC
XX The sequence encodes the entire 40 kD TNF inhibitor. The clone from
XX CC which the sequence was obtd. was isolated from a cDNA library
XX CC prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
XX CC gene can be inserted into expression vectors for prep'n. of TNF
XX CC inhibitor for use in the treatment of inflammatory and degenerative
XX CC diseases.
XX CC See also AAQ10878, AAQ10884 and AAQ10883.
XX CC
XX Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;
XX SQ

Query Match		44.4%;	Score 1159;	DB 12;	Length 2393;
Best Local Similarity		98.2%;	Pred. No. 1.1e-299;		
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		Gaps			
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QY	157	AATGTCACCTGCATCTGCTGAACGCTGTGTAGCAGCTCTGTACCACAGCTCTGACCAAGCTTCACAGTCTCTCCCT	216		
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QY	217	CAAGCCAGCTCCCAATATGGGAGACACAGATTCAGGCCCTTCGAGGTCCTCCGGAAGACAG	276		
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DB	1470	CCCAAGTTAAACAGGCCCGTGTGGGCTGTGCTGTAGCCAGAGTGTGGCTGAGCCCTGGCAGG	1529		
QY	457	ATGACCTCGGAAGGGGCCCTGTCTCCAGGCCCCCACTAGGACTCTGAGGCTCT	516		
DB	1530	ATGACCTCGGAAGGGG-CCTGTCTCTCCAGGCCCCCACTAGGACTCTGAGGCTCT	1588		
QY	517	TTCTGGGCCAAGTTCCTCTAGTGCCCTCCACAGCCGACGCTCCCTCTGACCTCGAGGCC	576		
DB	1589	TTCTGGGCCAAGTTCCTCTAGTGCCCTCCACAGCCGACGCTCCCTCTGACCTCGAGGCC	1648		
QY	577	AAGAGACAGGCGACGAGTTGGGGAAGGCTCTGCTGCCATGGTGTGTCCTCTCGGAAG	636		
DB	1649	AAGAGACAGGCGACGCGGTGTGGAAAGGCTCTGCTGCCATGGTGTGTCCTCTCGGAAG	1708		
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DB	1709	GCTGGCTGGGCATGGACGTCGCGGGCATGCTGGGGCAAGTCCCTGACTCTCTGTGACCTG	1768		
QY	697	CCCGGCCACGCTGCACCTGCCAGCCTGGCTTCGAGAGCCCTTGGGTFTTTGTTGTTGTTG	756		
DB	1769	CCCGGCCACGCTGCACCTGCCAGCCTGGCTTCGAGAGCCCTTGGGTFTTTGTTGTTGTTG	1828		
QY	757	TTTGTGTTGTTGTTGTTTCTCCCTCGGGCTCTG-CACAGCTCTGCTCCAGAAACC	815		
DB	1829	TTTGTGTTGTTGTTGTTTCTCCCTCGGGCTCTGCCCCAGCTCTGCTCCAGAAACC	1888		

tumour necrosis factor (TNF) receptor ligand - used to increase

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 628.284 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
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2	2493	95.4	3683	24 ABK83997	Human cDNA differe
3	2493	95.4	3683	24 ABK65877	Lung cancer relate
4	2493	95.4	3683	24 ABK33465	Human TNF receptor
5	2493	95.4	3683	24 ABK33466	Human TNF receptor
6	2493	95.4	3683	24 ABK33467	Human TNF receptor
7	1423	54.5	2339	12 AAQ10956	Encodes human 75kD
8	1423	54.5	2339	20 AAZ09171	Human tumour necro
9	1423	54.5	2339	22 AAH48860	Human TNFBP-associ

SUMMARIES

10	1171	44.8	2394	22 AAC83951	Human 40 kDa TNF 1
11	1159	44.4	2393	12 AAQ10907	40kD TNF inhibitor
12	1022.8	39.1	2224	16 AAQ89544	p75 Tumour Necrosi
c 13	613.2	23.5	733	24 ABK83541	Human cDNA differe
14	453	17.3	1641	14 AAQ49931	TNF-R cDNA. Homo
15	453	17.3	1641	15 AAQ45224	Sequence encoding
16	441	16.9	1640	12 AAQ10990	Partial sequencing o
c 17	337.8	12.9	455	22 AAH83437	Human ovarian tumo
c 18	336	12.9	336	22 AAQ24803	Human ovarian PCR-
c 19	245.2	9.4	618	22 AAQ62220	Human immune/haema
c 20	244.8	9.4	119950	20 AAQ90201	Human immune/haema
c 21	244	9.3	27154	22 AAQ05708	Human vesl gene.
c 22	243.2	9.3	2932	13 AAQ25388	Human reproductive
c 23	243.2	9.3	2932	20 AAQ23161	Human thromboxane
c 24	243.2	9.3	2932	20 AAQ23162	Human endothelial
c 25	243.2	9.3	2932	23 AAQ65879	DNA encoding novel
c 26	243.2	9.3	2932	24 ABK83654	Human cDNA differe
c 27	242.6	9.3	2500	22 ABK94360	Human full-length
c 28	242	9.3	589	22 ABK73475	Human immune/haema
c 29	241.8	9.3	14848	22 ABK15454	Human nervous syst
c 30	241.8	9.3	17542	22 ABK15453	Human nervous syst
c 31	241.2	9.2	122888	24 ABK83569	Human cDNA differe
c 32	241	9.2	3234	16 AAQ92781	Human thymopoietin
c 33	241	9.2	4125	22 ABK84260	Human immune/haema
c 34	241	9.2	4129	22 ABK84261	Human immune/haema
c 35	240.8	9.2	22609	22 AAQ35781	Human musculoskele
c 36	240.8	9.2	32193	22 AAQ35782	Human musculoskele
c 37	240.2	9.2	827	24 ABQ88849	Human prostate exp
38	240	9.2	240	24 ABK45619	cDNA encoding colo
39	240	9.2	26390	22 AAQ65971	Human immune/haema
c 40	240	9.2	27869	22 ABK19635	Human nervous syst
c 41	240	9.2	27869	22 ABK66517	Human immune/haema
c 42	239.8	9.2	825	22 AAQ86384	Human immune/haema
c 43	239.8	9.2	43599	24 ABK84242	Human cDNA differe
c 44	239.6	9.2	1296	19 AAQ29031	Human protein comp
c 45	239.6	9.2	12500	22 AAQ77971	Human immune/haema

ALIGNMENTS

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XX	AAAA9207	
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XX	AAAA9207	
DT	22-NOV-2000	(first entry)
XX	Human tumour necrosis factor alpha receptor 2 gene exon 10.	
DE	Human tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;	
KW	Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;	
KW	osteoporosis; ds.	
XX	Homo sapiens.	
OS	Homo sapiens.	
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FT		/product= "TNFR2"
FT		/partial
FT	allele	replace (593,A), (598,G), (620,T)
FT		/*tag= b
FT	allele	/label= allele_1
FT		replace (593,A), (598,T), (620,T)
FT		/*tag= c
FT	allele	/label= allele_2
FT		replace (593,G), (598,T), (620,C)
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FT	allele	/label= allele_3
FT		replace (593,G), (598,T), (620,T)
FT		/*tag= e
FT		/label= allele_4

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XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB: ABG23902.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1: SEQ ID NO 23893; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 448 BP; 86 A; 141 C; 130 G; 91 T; 0 other;

Query Match 80.9%; Score 17.8; DB 23; Length 448;
Best Local Similarity 90.5%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACTCA 21
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Db 167 GTGAAGTCAAGATGACCTCA 147

RESULT 9
ID AAS88094/c
XX AAS88094 standard; cDNA; 474 BP.
XX AC AAS88094;
XX DT 13-FEB-2002 (first entry)
XX DE DNA encoding novel human diagnostic protein #23898.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.

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XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR P-PSDB: ABG23907.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 1: SEQ ID NO 23898; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. AAS64197-AAS94564 represent novel human
XX CC diagnostic coding sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 474 BP; 88 A; 158 C; 130 G; 98 T; 0 other;

Query Match 80.9%; Score 17.8; DB 23; Length 474;
Best Local Similarity 90.5%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACTCA 21
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Db 266 GTGAAGTCAAGATGACCTCA 246

RESULT 10
ID AAD22561
XX AAD22561 standard; DNA; 651 BP.
XX AC AAD22561;
XX DT 29-JAN-2002 (first entry)
XX DE Human FDRG (fibrinogen domain related) related DNA.
XX KW Human; FDRG; fibrinogen domain related protein; signal transduction;
XX KW homeostasis; thermogenesis; adiposity; lipolysis; lipogenesis; obesity;
XX KW vasculogenesis; angiogenesis; wound healing; cardiovascular disorder;
XX KW hyperinsulinaemia; diabetes; atherosclerosis; cancer; tumour; cachexia;
XX KW gene therapy; anorectic; vulnery; immunomodulator; cytostatic;
XX KW appetite; glucose metabolism; ds.
XX OS Homo sapiens.
XX FH Key
XX CDS Location/Qualifiers
XX FT 1..651
XX FT /*tag= a
XX FT /product= "Human FDRG (fibrinogen domain related)
XX FT related protein"
XX FT /note= "CDS does not include both start and stop
XX FT codon"
XX FT /partial

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XX PN WO200177151-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-US11400.
XX PR 07-APR-2000; 2000US-0546547.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA (DAND ) DANA FARBEN CANCER INST INC.
XX PI Holtzman DA, Spiegelman BM, Yoon CH;
XX XX WPI: 2002-010893/01.
XX DR P-PSDB; AAE13522.
XX XX
XX PT Novel fibrinogen domain related polypeptides and polynucleotides useful
XX PT as modulating agents in regulating angiogenesis, metabolism-related
XX PT processes and for treating hematopoietic and proliferative disorders -
XX XX Disclosure; Page 147; 169pp; English.
XX CC The invention relates to novel FDRG (fibrinogen domain related) proteins
XX CC and their corresponding nucleic acids. FDRG or its modulator is useful
XX CC for activation of FDRG-dependent signal transduction pathway, modulation
XX CC of angiogenesis, haematopoiesis, development or differentiation of a
XX CC FDRG-expressing cell (e.g. mediation of growth and/or differentiation
XX CC of adipocytes, white adipocytes or brown adipocytes), proliferation,
XX CC development or differentiation of non-FDRG-expressing cell, homeostasis
XX CC of a (non) FDRG-expressing cell, insulin sensitivity and/or insulin
XX CC responsiveness, insulin secretion, cell recruitment, glucose metabolism,
XX CC maintenance of energy homeostasis (e.g. regulating the balance and/or
XX CC imbalance between energy storage and energy expenditure, for e.g.
XX CC increasing/decreasing energy expenditure), regulation of adaptive
XX CC thermogenesis (e.g. regulation of the biogenesis of mitochondria,
XX CC expression of mitochondrial enzymes, expression of uncoupling proteins),
XX CC regulation of adiposity, lipolysis, lipogenesis, modulation of the
XX CC efficiency of energy storage, regulation of appetite, vasculogenesis,
XX CC tumour angiogenesis, wound healing and expansion/reduction of tumour and
XX CC fat mass. FDRG or its modulator is useful for regulating, preventing
XX CC and/or treating obesity, diseases or disorders that accompany obesity
XX CC (e.g. cardiovascular disorders), metabolic abnormalities typical of
XX CC obesity (hyperinsulinaemia), diabetes, disorders of energy homeostasis,
XX CC insulin resistance, disorders associated with lipid metabolism (e.g.
XX CC cachexia), atherosclerosis, disorders associated with abnormal
XX CC vasculogenesis (e.g. cancers, including cancers of the epithelia e.g.
XX CC carcinomas of the pancreas, stomach, liver, secretory glands, bladder,
XX CC lung, breast, skin), reproductive tract and cancers of the
XX CC haematopoietic, immune system and nervous system. FDRG DNA is used in
XX CC gene therapy. The present sequence is human FDRG related DNA.
XX XX
XX SQ Sequence 651 BP; 129 A; 203 C; 203 G; 116 T; 0 other;
XX
XX Query Match 80.9%; Score 17.8; DB 24; Length 651;
XX Best Local Similarity 90.5%; Pred. No. 83;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX OY 1 GTGATCTCGAAGTCACTCA 21
XX 1111 1111111111 1111
XX
XX Db 91 GTGAAGTCAAGATGACCTCA 111
XX
XX RESULT 11
XX AAD22560
XX ID AAD22560 standard; cDNA; 1143 BP.
XX AC AAD22560;
XX XX
XX XX 29-JAN-2002 (first entry)
XX
XX DE Human mature FDRG (fibrinogen domain related) protein encoding cDNA.
XX

```

```

KW Human: FDRG; fibrinogen domain related protein; signal transduction;
KW homeostasis; thermogenesis; adiposity; lipolysis; lipogenesis; obesity;
KW vasculogenesis; angiogenesis; wound healing; cardiovascular disorder;
KW hyperinsulinaemia; diabetes; atherosclerosis; cancer; tumour; cachexia;
KW gene therapy; anorectic; vulnery; immunomodulator; cytostatic;
KW appetite; glucose metabolism; ss.
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
XX FT CDS 1..1143
XX FT /*tag= a
XX FT /product= "Human mature FDRG (fibrinogen domain
XX FT related) protein"
XX
XX PN WO200177151-A2.
XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-US11400.
XX PR 07-APR-2000; 2000US-0546547.
XX XX
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PA (DAND ) DANA FARBEN CANCER INST INC.
XX
XX PI Holtzman DA, Spiegelman BM, Yoon CH;
XX XX
XX DR WPI: 2002-010893/01.
XX DR P-PSDB; AAE13521.
XX
XX PT Novel fibrinogen domain related polypeptides and polynucleotides useful
XX PT as modulating agents in regulating angiogenesis, metabolism-related
XX PT processes and for treating hematopoietic and proliferative disorders -
XX XX Claim 2; Fig 2; 169pp; English.
XX
XX CC The invention relates to novel FDRG (fibrinogen domain related) proteins
XX CC and their corresponding nucleic acids. FDRG or its modulator is useful
XX CC for activation of FDRG-dependent signal transduction pathway, modulation
XX CC of angiogenesis, haematopoiesis, development or differentiation of a
XX CC FDRG-expressing cell (e.g. mediation of growth and/or differentiation
XX CC of adipocytes, white adipocytes or brown adipocytes), proliferation,
XX CC development or differentiation of non-FDRG-expressing cell, homeostasis
XX CC of a (non) FDRG-expressing cell, insulin sensitivity and/or insulin
XX CC responsiveness, insulin secretion, cell recruitment, glucose metabolism,
XX CC maintenance of energy homeostasis (e.g. regulating the balance and/or
XX CC imbalance between energy storage and energy expenditure, for e.g.
XX CC increasing/decreasing energy expenditure), regulation of adaptive
XX CC thermogenesis (e.g. regulation of the biogenesis of mitochondria,
XX CC expression of mitochondrial enzymes, expression of uncoupling proteins),
XX CC regulation of adiposity, lipolysis, lipogenesis, modulation of the
XX CC efficiency of energy storage, regulation of appetite, vasculogenesis,
XX CC tumour angiogenesis, wound healing and expansion/reduction of tumour and
XX CC fat mass. FDRG or its modulator is useful for regulating, preventing
XX CC and/or treating obesity, diseases or disorders that accompany obesity
XX CC (e.g. cardiovascular disorders), metabolic abnormalities typical of
XX CC obesity (hyperinsulinaemia), diabetes, disorders of energy homeostasis,
XX CC insulin resistance, disorders associated with lipid metabolism (e.g.
XX CC cachexia), atherosclerosis, disorders associated with abnormal
XX CC vasculogenesis (e.g. cancers, including cancers of the epithelia e.g.
XX CC carcinomas of the pancreas, stomach, liver, secretory glands, bladder,
XX CC lung, breast, skin), reproductive tract and cancers of the
XX CC haematopoietic, immune system and nervous system. FDRG DNA is used in
XX CC gene therapy. The present sequence is a cDNA encoding human mature
XX CC FDRG protein.
XX XX
XX SQ Sequence 1143 BP; 232 A; 373 C; 356 G; 182 T; 0 other;
XX
XX Query Match 80.9%; Score 17.8; DB 24; Length 1143;
XX Best Local Similarity 90.5%; Pred. No. 91;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 GTGATCTGCAAGATGAACCTCA 21
 DB 565 GTGAACTGCAAGATGAACCTCA 585

RESULT 12
 AAD22559
 ID AAD22559 standard; cDNA; 1218 BP.
 XX
 AC AAD22559;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human FDRG (fibrinogen domain related) protein encoding cDNA fragment.
 XX
 KW Human; FDRG; fibrinogen domain related protein; signal transduction;
 KW homeostasis; thermogenesis; adiposity; lipolysis; lipogenesis; obesity;
 KW vasculogenesis; angiogenesis; wound healing; cardiovascular disorder;
 KW hyperinsulinaemia; diabetes; atherosclerosis; cancer; tumour; cachexia;
 KW gene therapy; anorectic; vulnary; immunomodulator; cytostatic;
 KW appetite; glucose metabolism; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200177151-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-US11400.
 XX
 PR 07-APR-2000; 2000US-0546547.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Holtzman DA, Spiegelman BM, Yoon CH;
 XX
 DR WP1; 2002-010893/01.
 XX
 PT Novel fibrinogen domain related polypeptides and polynucleotides useful
 PT as modulating agents in regulating angiogenesis, metabolism-related
 PT processes and for treating hematopoietic and proliferative disorders -
 XX
 XX Claim 2; Page 142-143; 169pp; English.
 XX
 CC The invention relates to novel FDRG (fibrinogen domain related) proteins
 CC and their corresponding nucleic acids. FDRG or its modulator is useful
 CC for activation of FDRG-dependent signal transduction pathway, modulation
 CC of angiogenesis, hematopoiesis, development or differentiation of a
 CC FDRG-expressing cell (e.g. mediation of growth and/or differentiation
 CC of adipocytes, white adipocytes or brown adipocytes), proliferation,
 CC development or differentiation of non-FDRG-expressing cell, homeostasis
 CC of a (non) FDRG-expressing cell, insulin sensitivity and/or insulin
 CC responsiveness, insulin secretion, cell recruitment, glucose metabolism,
 CC maintenance of energy homeostasis (e.g. regulating the balance and/or
 CC imbalance between energy storage and energy expenditure, for e.g.
 CC increasing/decreasing energy expenditure), regulation of adaptive
 CC thermogenesis (e.g. regulation of the biogenesis of mitochondria,
 CC expression of mitochondrial enzymes, expression of uncoupling proteins),
 CC regulation of adiposity, lipolysis, lipogenesis, modulation of the
 CC efficiency of energy storage, regulation of appetite, vasculogenesis,
 CC tumour angiogenesis, wound healing and expansion/reduction of tumour and
 CC fat mass. FDRG or its modulator is useful for regulating, preventing
 CC and/or treating obesity, diseases or disorders that accompany obesity
 CC (e.g. cardiovascular disorders), metabolic abnormalities typical of
 CC obesity (hyperinsulinaemia), diabetes, disorders of energy homeostasis,
 CC insulin resistance, disorders associated with lipid metabolism (e.g.
 CC cachexia), atherosclerosis, disorders associated with abnormal
 CC vasculogenesis (e.g. cancers, including cancers of the epithelia e.g.
 CC carcinomas of the pancreas, stomach, liver, secretory glands, bladder,
 CC lung, breast, skin), reproductive tract and cancers of the
 CC haematopoietic, immune system and nervous system. FDRG DNA is used in
 CC gene therapy. The present sequence is human FDRG cDNA fragment.

XX
 SQ Sequence 1218 BP; 241 A; 401 C; 383 G; 193 T; 0 other;
 Query Match 80.9%; Score 17.8; DB 24; Length 1218;
 Best Local Similarity 90.5%; Pred. No. 92;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTGATCTGCAAGATGAACCTCA 21
 DB 640 GTGAACTGCAAGATGAACCTCA 660
 RESULT 13
 AA297139
 ID AA297139 standard; DNA; 1221 BP.
 XX
 AC AA297139;
 XX
 DT 19-APR-2000 (first entry)
 XX
 DE Human gene 75 DNA sequence, SEQ ID NO:448.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; gene 75; chromosome 19; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO9966041-A1.
 XX
 PD 23-DEC-1999.
 XX
 PF 15-JUN-1999; 99WO-US13418.
 XX
 PR 16-JUN-1998; 98US-0089507.
 PR 16-JUN-1998; 98US-0089508.
 PR 16-JUN-1998; 98US-0089509.
 PR 16-JUN-1998; 98US-0089510.
 PR 22-JUN-1998; 98US-0090112.
 PR 22-JUN-1998; 98US-0090113.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
 PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsu G;
 XX
 DR WPI; 2000-106100/09.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Disclosure; Page 159; 586pp; English.
 XX
 CC AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 CC AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC e.g., by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 94 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin

CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
CC disorders, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The sequences shown in AAY86334 to AAY86585 represent fragments of the
CC secreted proteins, and the sequences shown in AAZ97138 and AAZ97139
CC represent gene 75 nucleotide sequences.
XX
SQ Sequence 1221 BP; 242 A; 400 C; 385 G; 194 T; 0 other;
Query Match 80.9%; Score 17.8; DB 21; Length 1221;
Best Local Similarity 90.5%; Pred. NO. 92;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GTGATCTGCAAGATGAACCTCA 21
||||| ||||||| |||||
DB 640 GTGAAGTGCAGATGACCTCA 660
RESULT 14
AAZ97132
ID AAZ97132 standard; cDNA; 1379 BP.
XX
AC AAZ97132;
XX
DT 19-APR-2000 (first entry)
XX
DE Human secreted protein gene 75 cDNA clone HDRM182, SEQ ID NO:124.
XX
KW Human: secreted protein; cancer; tumour; developmental abnormality;
KW foetal disease; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; ds.
XX
XX Homo sapiens.
XX
XX WO9966041-A1.
XX
XX 23-DEC-1999.
XX
XX 15-JUN-1999; 99WO-US13418.
XX
XX 16-JUN-1998; 98US-0089507.
XX PR 16-JUN-1998; 98US-0089508.
XX PR 16-JUN-1998; 98US-0089509.
XX PR 16-JUN-1998; 98US-0089510.
XX PR 22-JUN-1998; 98US-0090112.
XX PR 22-JUN-1998; 98US-0090113.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ni J., Rosen CA, Wei Y, Young PE, Florence KA;
XX Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;
XX Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsuouli G;
XX
XX WPI: 2000-106100/09.
XX
XX P-PSDB: AAY86328.
XX
XX New isolated human genes and the secreted polypeptides they encode,
XX useful for diagnosis and treatment of e.g. cancers, neurological
XX disorders, immune diseases, inflammation or blood disorders -
XX
XX Claim 1: Page 384; 586pp; English.
XX
XX AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes.
XX AAZ97215 to AAY86333 are the secreted proteins encoded by the 94 human
XX genes. This sequence represents a fragment of one of the human secreted
XX proteins. The genes and their corresponding secreted polypeptides are
XX useful for preventing, treating or ameliorating medical conditions,
XX e.g., by protein or gene therapy. Also pathological conditions can be
XX diagnosed by determining the amount of the new polypeptides in a sample

CC or by determining the presence of mutations in the new genes. Specific
CC uses are described for each of the 94 genes, based on which tissues they
CC are most highly expressed in, and include developing products for the
CC diagnosis or treatment of cancer, tumours, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
CC disorders, schizophrrenia, arthritis, asthma, psoriasis, sepsis, skin
CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
CC disorders, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The sequences shown in AAY86334 to AAY86585 represent fragments of the
CC secreted proteins.
XX
SQ Sequence 1379 BP; 313 A; 398 C; 431 G; 237 T; 0 other;
Query Match 80.9%; Score 17.8; DB 21; Length 1379;
Best Local Similarity 90.5%; Pred. NO. 94;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GTGATCTGCAAGATGAACCTCA 21
||||| ||||||| |||||
DB 273 GTGAAGTGCAGATGACCTCA 293
RESULT 15
ABQ88100
ID ABQ88100 standard; cDNA; 1413 BP.
XX
AC ABQ88100;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human osteoblast differentiation related cDNA SEQ ID NO 7.
XX
XX Human: osteoblast; stem cell differentiation; bone tissue deposition;
XX osteoporosis; osteopathic; ss.
XX
XX Homo sapiens.
XX
XX WO200250301-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US48276.
XX
XX 18-DEC-2000; 2000US-255882P.
XX PR 24-APR-2001; 2001US-285691P.
XX
XX (GENE-) GENE LOGIC INC.
XX PA (PROC) PROCTER & GAMBLE CO.
XX
XX Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
XX Mertz L;
XX
XX WPI: 2002-557663/59.
XX
XX Use of genes and their expression profiles associated with osteoblast
XX differentiation for screening modulators bone formation, for diagnosing
XX or treating e.g. osteoporosis, or as markers for the differentiation
XX process -
XX
XX Claim 1; SEQ ID NO 7; 78pp + Sequence Listing; English.
XX
XX The invention relates to genes and their expression profiles are used
XX for:
XX (a) screening modulators of precursor stem cell differentiation into
XX osteoblasts, or bone tissue deposition;
XX (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
XX osteoblast formation or osteoporosis; or
XX (c) treating or monitoring treatment of the conditions cited in (b), or
XX monitoring the progression of bone tissue deposition.
XX Specific conditions include postmenopausal osteoporosis, glucocorticoid
XX osteoporosis or male osteoporosis, osteopenia, osteodystrophy,

CC drug-induced abnormalities in bone formation or bone loss, conditions
 CC that involve altered bone metabolism (e.g. idiopathic juvenile
 CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
 CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
 CC osteoblast differentiation associated cDNA marker of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 1413 BP; 278 A; 463 C; 444 G; 228 T; 0 other;

Query Match 80.9%; Score 17.8; DB 24; Length 1413;
 Best Local Similarity 90.5%; Pred. No. 94;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGAACCTCA 21
 ||||| ||||| ||||| ||||| |||||
 Db 704 GTCACTGCAAGATGACCTCA 724

Search completed: December 5, 2002, 23:29:56
 Job time : 39.2898 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 : Search time 42.1061 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937a-2

Perfect score: 22

Sequence: 1 gtgatctgcaagatgaactcac 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	18.8	85.5	482	17	AQ817730 HS-5250_B
2	17.8	80.9	78	13	BJ062060 BJ062060
3	17.8	80.9	240	9	AV249962 AV249962
4	17.8	80.9	305	14	M62290 EST00364 Hi
5	17.8	80.9	353	14	T08223 EST06114 In
6	17.8	80.9	400	12	BF023606 5 Human H

7 17.8 80.9 424 14 T33835
8 17.8 80.9 484 9 AA122061
c 9 17.8 80.9 493 10 BE215937
10 17.8 80.9 509 14 BM967237
c 11 17.8 80.9 521 17 BH360315
12 17.8 80.9 527 14 BM967022
13 17.8 80.9 561 13 BM179919
c 14 17.8 80.9 576 9 AJ498267
15 17.8 80.9 586 17 BH351116
c 16 17.8 80.9 608 13 BJ107879
17 17.8 80.9 610 9 AI556475
c 18 17.8 80.9 627 12 BF005034
19 17.8 80.9 631 10 AW956861
c 20 17.8 80.9 644 17 BH033878
21 17.8 80.9 680 9 AL648363
c 22 17.8 80.9 702 12 BG583307
23 17.8 80.9 812 17 A2703920
24 17.8 80.9 841 14 B0881023
25 17.8 80.9 859 17 CNS03GKF
26 17.8 80.9 893 13 B1192811
c 27 17.4 79.1 163 9 AA192559
c 28 17.4 79.1 228 17 AQ580761
c 29 17.4 79.1 321 10 AW382482
c 30 17.4 79.1 336 12 BE708615
c 31 17.4 79.1 344 14 Z29781
c 32 17.4 79.1 349 10 AW509663
33 17.4 79.1 364 12 BF989328
c 34 17.4 79.1 393 14 BQ359828
c 35 17.4 79.1 398 10 BE168428
c 36 17.4 79.1 467 10 AW699768
c 37 17.4 79.1 509 13 BJ180510
c 38 17.4 79.1 512 13 BJ159235
39 17.4 79.1 518 13 BJ172933
c 40 17.4 79.1 520 9 AL120881
41 17.4 79.1 539 10 AW382320
42 17.4 79.1 561 10 AV830290
c 43 17.4 79.1 561 13 BJ172163
c 44 17.4 79.1 569 13 BJ187317
c 45 17.4 79.1 574 13 BJ193124

ALIGNMENTS

RESULT 1
AQ817730
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

AQ817730
HS_5250_B1_C07_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate-826 Col-13 Row=F, DNA sequence.
AQ817730
GI:5780123
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 482)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallaceu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (inforesgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 826 row: F column: 13
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 482.
 Location/Qualifiers
 1..482

FEATURES

source

1..482

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-826 Col-13 Row-F"
 /clone_lib="RPC1-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
 98 a 137 c 107 g 131 t 9 others

BASE COUNT

ORIGIN

Query Match 85.5%; Score 18.8; DB 17; Length 482;
 Best Local Similarity 90.9%; Pred. No. 3.le+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTAC 22
 ||| ||||| ||||| ||||| |||||

Db 308 GTGGTCTGCAAGATGAACCTAC 329

RESULT 2

LOCUS

DEFINITION BJ062060 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL074006 5', mRNA sequence. EST 11-DEC-2001

ACCESSION BJ062060

VERSION BJ062060.1 GI:17499724

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Ambiphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.

1 (bases 1 to 78)

Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara

,Y.

Expressed genes in X. laevis embryo

Unpublished (2001)

Contact: Tadasi Shin-I

Center for Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1..78

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="XL074006"

/clone_lib="NIBB Mochii normalized Xenopus tailbud

library"

/tissue_type="whole embryo"

/dev_stage="stage 25"

/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs

were oligo-dT primed and directionally cloned. Staging

according to Nieuwkoop and Faber. Library is subtracted

and was constructed by N. Garrett and A.M. Zorn,

(Wellcome/CRC Institute)."

23 a 17 c 16 g 20 t 2 others

BASE COUNT

ORIGIN

Query Match 80.9%; Score 17.8; DB 13; Length 78;
 Best Local Similarity 90.5%; Pred. No. 4.6e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGATCTGCAAGATGAACCTAC 22
 || |||| ||||| ||||| |||||

Db 38 TGCTCTGGAAGATGAACCTAC 58

RESULT 3

AV249962/c

LOCUS

DEFINITION

AV249962 RIKEN full-length enriched, 0 day neonate head Mus

musculus cDNA clone 483420C07 3', similar to X84797 M. musculus mRNA

similar to human hematopoietic specific protein 1, mRNA sequence.

AV249962

AV249962.1 GI:6237421

EST.

house mouse.

Mus musculus

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 240)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,

Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,

Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai

,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,

Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,

Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata

,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,

Suzuki,H., Takahashi,F., Tateo,M., Tomimaga,N., Tsunoda,Y.,

Wataniki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,

Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al. 1999)

Unpublished (1999)

Contact: Yoshihide Hayashizaki

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Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>,

Sasaki,N., Izawa,M., Wataniki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,

Matsuyama,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki

,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

Location/Qualifiers

1..240

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="483420C07"

/clone_lib="RIKEN full-length enriched, 0 day neonate

head"

/sex="mixed"

/tissue_type="head"

/dev_stage="0 day neonate"

/lab_host="DH10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was

FEATURES

source


```
1. .424
/organism="Homo sapiens"
/db_xref="ATCC (inhost):104464"
/db_xref="taxon:9606"
/clone_lib="Human Brain"
```

BASE COUNT	103 a	120 c	127 g	69 t	5 others					
ORIGIN										
Query Match 80.9%; Score 17.8; DB 14; Length 424;										
Best Local Similarity 90.5%; Pred. No. 8.4e+02;										
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;										
QY	1	GTGATCTCGAAGATGA	ACTCA	21						
Db	364	GTGAAC	TGCAAGATGACCTCA	384						

RESULT 8
AA122061
LOCUS

DEFINITION
 zK93b12.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
 IMAGE:490367 5' similar to SW:FIBG_PETMA P04115 FIBRINOGEN GAMMA
 CHAIN PRECURSOR. ; mRNA sequence.

KEYWORDS
 EST.
 SOURCE
 ORGANISM
 EST.
 SOURCE
 ORGANISM

Eukaryotes; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 484)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags

REFERENCE

AUTHORS

TITLE

JOURNAL

Genome Res. 6 (9), 807-828 (1996)
9704478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1646 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 427.
Location/Qualifiers
1. 484
/organism="Homo sapiens"
/db_xref="GDB:3804954"

```

/db_xref="taxon:9606"
/clone="IMAGE:490367"
/clone_lib="Soares_pregnant_uterus_NbHP0"
/sex="female"

```

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/dev_stage="adult"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: pT73-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AAGTCGAGAAATTCGCGCCCTTTTTTTTTTTTTTTTTT 3'],

```

BASE COUNT
ORIGIN

```

Query Match      80.9%; Score 17.8; DB 9; Length 484;
Best Local Similarity 90.5%; Pred. No. 8.8e-02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CTGATCTGCAAGATGAACCTCA 21
    |||| ||||| ||||| |||||
Db 44 CTGAACCTGCAAGATGACCTCA 64

RESULT 9
BE215937/c
LOCUS      BE215937
DEFINITION HV_CEB0008007f Hordeum vulgare seedling green leaf EST 23-OCT-2001
            HVCNDA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
            HV_CEB0008007f, mRNA sequence.
ACCESSION  BE215937
VERSION     BE215937.2 GI:13264649
KEYWORDS   EST.
SOURCE     Hordeum vulgare.
ORGANISM   Hordeum vulgare.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
            ; Triticeae; Hordeum.
            1 (bases 1 to 493)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Chol
,D.W., Fenton,R.D., Oates R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library
Unpublished (2001)
On Jul 3, 2000 this sequence version replaced gi:8903549.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 447
Seq primer: AATTAACCTCACTAAAGCG
High quality sequence stop: 488.

FEATURES             source
    1..493
        /organism="Hordeum vulgare"
        /cultivar="C116151 (Mla6)"
        /db_xref="taxon:4513"
        /clone="HV_CEB0008007f"
        /clone_lib="Hordeum vulgare seedling green leaf EST
        library HVCNDA0005 (Blumeria challenged)"
        /tissue_type="seedling green leaf"
        /lab_host="SOLR"
        /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
        C.I. 16151 (Mla6) plants were greenhouse grown in the R
        Wise lab at Iowa State University, Ames, IA; 7 day old
        green seedlings were challenged with isolate 5874 (AvrMla6
        ) of Blumeria graminis f. sp. hordei, and leaves were
        harvested 20 and 24 hr post-inoculation and snap frozen;
        uninoculated leaves were harvested 20 hr post-inoculation
        (Wei, Wise). In the TJ Close lab at the University of
        California, Riverside, total RNA was prepared from each
        sample pool, equal quantities of all three RNA pools were
        combined, poly(A) RNA was purified from the mixture, one
        pfu were in vivo excised to give pBluescript SK(-) cDNA
        phagemids (Choi, Close). Phagemids were plated and picked
        at the Clemson University Genomics Institute (CUGI) (Begum
        , Palmer, Frisch, Atkins and Wing). Plasmid DNA
        preparations, DNA sequencing and sequence analysis were
        performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
        , Rambo, Main). The sequence has been trimmed to remove
        vector sequence and contains a minimum of 100 bases of

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phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html).
BASE COUNT      115 a 148 c 143 g 86 t 1 others
ORIGIN

```

```

Query Match      80.9%; Score 17.8; DB 10; Length 493;
Best Local Similarity 90.5%; Pred. No. 8.9e-02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 GTGATCTGCAAGATGAACCTCA 21
    ||||| ||||| ||||| |||||
Db 427 GTGATCTCAAGAGGAACCTCA 407

```

```

RESULT 10
BM967237
LOCUS      BM967237
DEFINITION ij32c02.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
            CDNA clone IMAGE:6136322 5' similar to TR:Q9Y5B3 Q9Y5B3
            ANGIOPOIETIN-RELATED PROTEIN. ;, mRNA sequence.
ACCESSION  BM967237
VERSION     BM967237.1 GI:19561026
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 509)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blinston,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.,
Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: ij32c02.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohph.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 445.

```

```

FEATURES             source
    1..509
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:6136322"
        /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
        /sex="Both"
        /tissue_type="Islets of Langerhans"
        /dev_stage="Adult"
        /lab_host="DH10B"
        /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
        Site_2: Sal I; Starting library constructed using
        SuperScript Plasmid Library kit (Life Technologies). cDNA
        made by oligo-dT priming. Size-selected by column
        fractionation; average insert size 1.08 kb. Library was
        amplified once on solid support and plasmid DNA from

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library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 99 a 161 c 161 g 88 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 14; Length 509;
Best Local Similarity 90.5%; Pred. No. 9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGATCTGCAAGATGAACCTCA 21

||||| ||||| ||||| ||||| |||||

Db 23 GTGAAGTGCAGATGACCTCA 43

RESULT 11
BH360315/C

LOCUS

DEFINITION BH360315 521 bp DNA linear GSS 03-DEC-2001
CH230-107F8.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-107F8, DNA sequence.

ACCESSION BH360315

VERSION BH360315.1

KEYWORDS GI:17291049

SOURCE GSS.

ORGANISM Norway rat.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 521)

Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,

A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de

Jong, P., and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment

Unpublished (1999)

Other_GSSs: CH230-107F8.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html

Plate: 107 row: F column: 8

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..521

/organism="Rattus norvegicus"

/strain="BN/SsNHsd/MCW"

/db_xref="taxon:10116"

/clone="CH230-107F8"

/clone_lib="CHORI-230 Segment 1"

/sex="Female"

/cell_type="Brain"

/note="vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;

CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by

Pieter de Jong"

BASE COUNT 80 a 106 c 127 g 208 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 17; Length 521;
Best Local Similarity 90.5%; Pred. No. 9e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTGATCTGCAAGATGAACCTCA 21

||||| ||||| ||||| ||||| |||||

Db 462 GTGACCTGCATGATGAACCTCA 442

RESULT 12

BH967022

LOCUS

DEFINITION BH967022 527 bp mRNA linear EST 29-APR-2002

ij29d10.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens

CDNA clone IMAGE:6136003 5' similar to TR:Q9Y5B3 Q9Y5B3

ANGIOPOIETIN-RELATED PROTEIN.; mRNA sequence.

ACCESSION BH967022

VERSION BH967022.1

KEYWORDS GI:19560624

SOURCE EST.

ORGANISM human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 527)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, F., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas

, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.

, Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other_ESTs: ij29d10.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Juliana Brown

(brown@fas.harvard.edu)

Seq primer: -40Rp from Gibco

High quality sequence stop: 451.

Location/Qualifiers

1..527

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6136003"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;

Site_2: Sal 1; Starting library constructed using

SuperScript Plasmid Library kit (Life Technologies). cDNA

made by oligo-dr priming. Size-selected by column

fractionation; average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from

library was prepared. The library DNA was normalized by

method #4 from Bonaldo, Lennon, and Soares 1996 Genome

Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product

representing library inserts and hybridized to an EcoT of

20. Single-stranded (unhybridized) plasmids were isolated

by hydroxyapatite chromatography and used to make this

library."

BASE COUNT 105 a 163 c 166 g 93 t

ORIGIN

Query Match 80.9%; Score 17.8; DB 14; Length 527;
Best Local Similarity 90.5%; Pred. No. 9.1e+02;

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Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
Db 23 GTCAACTGCAAGATGAACCTCA 43

RESULT 13
LOCUS BM179919
DEFINITION dail3d02.yl NICHD XGC Emb4 Xenopus laevis cDNA clone IMAGE:4959386
5' similar to SW:GPS1_RAT P97834 G PROTEIN PATHWAY SUPPRESSOR 1 ;
mRNA sequence.
ACCESSION BM179919
VERSION BM179919.1 GI:17403990
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 561)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 447.
FEATURES
    source
        location/Qualifiers
            1..561
                /organism="Xenopus laevis"
                /db_xref="taxon:8355"
                /clone="IMAGE:4959386"
                /clone_lib="NICHD XGC Emb4"
                /dev_stage="embryo, stage 31-32"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site_1:
                NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo
                dT. Average insert size 2.1 kb. Constructed by Life
                Technologies. Note: This is a Xenopus Gene Collection (XGC
                ) library."
BASE COUNT 145 a 128 c 121 g 167 t
ORIGIN
Query Match 80.9%; Score 17.8; DB 13; Length 561;
Best Local Similarity 90.5%; Pred. No. 9.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCATCTGCAAGATGAACCTAC 22
Db 498 TCCTCTGGAAGATGAACCTAC 518

RESULT 14
LOCUS AJ498267/c
DEFINITION AJ498267 MTP0SE Medicago truncatula cDNA clone mt--acc955202h09,
mRNA sequence.
ACCESSION AJ498267
VERSION AJ498267.1 GI:22088710
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 576)
Firnhaber, C., Bartelsmeier, V., Meyer, F., Bartels, D., Bekel, T.,
Linke, B., Puehler, A. and Kuester, H.
Determination of transcript sequences from developing pods
including seeds of Medicago truncatula genotype Al7
Unpublished (2002)
Contact: Kuester H
Lehrstuhl fuer Genetik
Universitaet Bielefeld
Postfach 100131, D-33501 Bielefeld, Germany.
FEATURES
    source
        location/Qualifiers
            1..576
                /organism="Medicago truncatula"
                /db_xref="taxon:3880"
                /clone="mt--acc955202h09"
                /clone_lib="MTP0SE"
                /tissue_type="pods including seeds"
                /dev_stage="different stages of development"
                /note="Vector: pGEM-T; Site_1: PstI; Site_2: SphI;
                genotype Al7; cDNA was prepared from polyA+ enriched RNA
                from developing pods including seeds harvested at
                different stages of development. The cDNA was
                directionally ligated by Medigenomix into the pGEM-T
                vector from Promega using GCATGCCGCGAGCGCCGACATG and
                CTCAGGCCATTATGCCGG adapters. Plasmids containing cDNA
                inserts were propagated in E. coli DH10B cells."
BASE COUNT 139 a 114 c 133 g 190 t
ORIGIN
Query Match 80.9%; Score 17.8; DB 9; Length 576;
Best Local Similarity 90.5%; Pred. No. 9.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TGATCTGCAAGATGAACCTAC 22
Db 315 TGAGCTGCAAGATGAACACAC 295

RESULT 15
LOCUS BH351116/c
DEFINITION BH351116 586 bp DNA linear GSS 03-DEC-2001
CH230-198M8, TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-198M8, DNA sequence.
ACCESSION BH351116
VERSION BH351116.1 GI:17281850
KEYWORDS GSS.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 586)
Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn,
A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.W.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
Other_GSSs: CH230-198M8.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@email.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or_ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

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Plate: 198 row: M column: 8
Seq primer: SP6
Class: BAC ends.
FEATURES
    source
        Location/Qualifiers
            1..586
                /organism="Rattus norvegicus"
                /strain="BN/SSNHsd/MCH"
                /db_xref="taxon:10116"
                /clone="CH230-198W8"
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                /cell_type="Brain"
                /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
                CHORI-230 Rat (BN/SSNHsd/MCH) BAC library produced by
                Pieter de Jong"
BASE COUNT      92 a   134 c   147 g   213 t
ORIGIN
Query Match      80.9%; Score 17.8; DB 17; Length 586;
Best Local Similarity 90.5%; Pred. No. 9.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Uy 1 GTGATCTGCAAGATGAATCA 21
    |||||
Db 447 GTGACCTGCATGATGAATCA 427

Search completed: December 6, 2002, 04:54:09
Job time : 56.1061 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 : Search time 1.14286 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-2

Perfect score: 22

Sequence: 1 gtgactctgcaagatgaactcac 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	17.8	80.9	1869	4	US-09-143-707-1
4	17.8	80.9	1869	4	US-09-202-089-1
5	17.8	80.9	1869	4	US-09-511-133-1
6	17.8	80.9	1869	4	US-09-690-169-1
7	17.8	80.9	1869	4	US-09-511-631-1
8	16.4	74.5	4440	3	US-07-792-600-1
9	16.4	74.5	4440	3	US-09-157-021-1
10	16.4	74.5	4440	3	US-09-156-842-1
11	16.4	74.5	5433	3	US-09-157-021-35
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13	16.2	73.6	571	4	US-09-404-879A-102
14	16.2	73.6	2045	1	US-08-379-926A-7
15	16.2	73.6	8533	1	US-07-846-181-6
16	16.2	73.6	8533	1	US-07-845-989-6
17	16.2	73.6	9763	3	US-08-973-273-1
18	15.8	71.8	499	1	US-07-935-311A-1
19	15.8	71.8	499	1	US-08-368-079-1
20	15.8	71.8	499	5	PCT-US93-07996-1
21	15.8	71.8	2840	5	PCT-US93-06251-64
22	15.8	71.8	4868	1	US-08-139-937-12
23	15.8	71.8	4868	5	PCT-US93-11310-12
24	15.8	71.8	8789	1	US-08-328-254-5
25	15.8	71.8	10136	1	US-08-353-700-2
26	15.8	71.8	10136	5	PCT-US95-16216-2
27	15.6	70.9	1272	2	US-08-972-258-1

c 28	15.6	70.9	1272	4	US-09-263-128-1	Sequence 1, Appli
c 29	15.6	70.9	1523	2	US-08-713-636-1	Sequence 1, Appli
c 30	15.6	70.9	2346	4	US-09-193-503B-4	Sequence 4, Appli
c 31	15.6	70.9	2346	4	US-09-193-503B-5	Sequence 5, Appli
c 32	15.6	70.9	2346	4	US-09-193-503B-8	Sequence 8, Appli
c 33	15.4	70.0	54	4	US-08-679-645-634	Sequence 634, App
c 34	15.4	70.0	55	1	US-07-869-380B-2	Sequence 2, Appli
c 35	15.4	70.0	64	1	US-07-869-380B-1	Sequence 1, Appli
c 36	15.2	69.1	685	3	US-08-881-094-14	Sequence 14, Appli
c 37	15.2	69.1	1991	4	US-08-235-836C-69	Sequence 69, Appli
c 38	15.2	69.1	1991	4	US-08-235-836C-77	Sequence 77, Appli
c 39	15.2	69.1	2665	4	US-08-971-089-5	Sequence 5, Appli
c 40	15.2	69.1	5211	1	US-08-447-411-1	Sequence 1, Appli
c 41	15.2	69.1	4403765	4	US-09-103-840A-2	Sequence 2, Appli
c 42	14.8	67.3	255	4	US-08-952-736B-3	Sequence 3, Appli
c 43	14.8	67.3	718	4	US-08-998-416-638	Sequence 638, App
c 44	14.8	67.3	948	4	US-09-134-001C-949	Sequence 949, App
c 45	14.8	67.3	996	1	US-07-757-390-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-934-494-1
; Sequence 1, Application US/08934494
; Patent No. 6030831
; GENERAL INFORMATION:
; APPLICANT: Gurney, Austin
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,494
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1869 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-934-494-1

Query Match 80.9%; Score 17.8; DB 3; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21

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Db 803 GTGAAGTGAAGATGAACCTCA 823

RESULT 2

US-09-143-068-1

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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,707
; FILING DATE: 28-Aug-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1078R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1869 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-09-143-707-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 GTGATCTGCAAGATGAACCTCA 21
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Db 803 GTGAAGTGCAGATGACCTCA 823

RESULT 4
US-09-202-089-1
; Sequence 1, Application US/09202089
; Patent No. 6348351
; GENERAL INFORMATION:
; APPLICANT: Genentech Inc.
; APPLICANT: Fong, Sherman
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth
; APPLICANT: Williams, Mickey
; TITLE OF INVENTION: Tie Ligand Homologues
; FILE REFERENCE: P1078P2(e)
; CURRENT APPLICATION NUMBER: US/09/202,089
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: PCT/US98/19094
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 08/934,494
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-202-089-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 GTGATCTGCAAGATGAACCTCA 21
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Db 803 GTGAAGTGCAGATGACCTCA 823

RESULT 5
US-09-511-133-1
; Sequence 1, Application US/09511133
; Patent No. 6372491
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

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; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; FILE REFERENCE: P1078R1C1
; CURRENT APPLICATION NUMBER: US/09/511,133
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: US 09/143,707
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 60/059,352
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-511-133-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
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Db 803 GTGAAGTCAAGATGACCTCA 823

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US-09-690-169-1
; Sequence 1, Application US/09690169
; Patent No. 6426218
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: TIE LIGANDS
; FILE REFERENCE: GENENT 58A2D2
; CURRENT APPLICATION NUMBER: US/09/690,169
; CURRENT FILING DATE: 2001-09-04
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 09/143,707
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/059,352
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-690-169-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
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RESULT 7

US-09-511-631-1
; Sequence 1, Application US/09511631
; Patent No. 6455496
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; FILE REFERENCE: P1078R1D1
; CURRENT APPLICATION NUMBER: US/09/511,631
; CURRENT FILING DATE: 2000-02-23
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 09/143,707
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: US 60/059,352

; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-511-631-1

Query Match 80.9%; Score 17.8; DB 4; Length 1869;
Best Local Similarity 90.5%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 803 GTGAAGTCAAGATGACCTCA 823

RESULT 8

US-07-792-600-1/c
; Sequence 1, Application US/07792600
; Patent No. 6008045
; GENERAL INFORMATION:
; APPLICANT: COPELAND, WILLIAM C.
; APPLICANT: WANG, TERESA S.-F.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC SYNTHESIS OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Peter G. Carroll
; STREET: 220 Montgomery Street, Suite 710
; CITY: San Francisco
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/792,600
; FILING DATE: 19911115
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: STDU-00097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4440 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-792-600-1

Query Match 74.5%; Score 16.4; DB 3; Length 4440;
Best Local Similarity 94.4%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGATCTGCAAGATGAACCT 19
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Db 2282 TGATCTGCAAGATGAACCT 2265

RESULT 9

US-09-157-021-1/c
; Sequence 1, Application US/09157021A
; Patent No. 6100023
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.

```

; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Design Assay
; FILE REFERENCE: STDU-03484
; CURRENT APPLICATION NUMBER: US/09/157,021A
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-157-021-1

Query Match      74.5%; Score 16.4; DB 3; Length 4440;
Best Local Similarity 94.4%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 10
US-09-156-842-1/c
; Sequence 1, Application US/09156842A
; Patent No. 6103473
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Screening
; FILE REFERENCE: STDU-03485
; CURRENT APPLICATION NUMBER: US/09/156,842A
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-156-842-1

Query Match      74.5%; Score 16.4; DB 3; Length 4440;
Best Local Similarity 94.4%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 11
US-09-157-021-35/c
; Sequence 35, Application US/09157021A
; Patent No. 6100023
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Design Assay
; FILE REFERENCE: STDU-03484
; CURRENT APPLICATION NUMBER: US/09/157,021A
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-157-021-35

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Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 12
US-09-156-842-35/c
; Sequence 35, Application US/09156842A
; Patent No. 6103473
; GENERAL INFORMATION:
; APPLICANT: Copeland, William C.
; APPLICANT: Wang, Teresa S. F.
; TITLE OF INVENTION: Drug Screening
; FILE REFERENCE: STDU-03485
; CURRENT APPLICATION NUMBER: US/09/156,842A
; EARLIER FILING DATE: 1998-09-18
; EARLIER FILING DATE: 1991-11-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-156-842-35

Query Match      74.5%; Score 16.4; DB 3; Length 5433;
Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 TGATCTGCAAGATGAAC 19
Db  2282 TGATCTGCAAAATGAAC 2265

RESULT 13
US-09-404-879A-102
; Sequence 102, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-404-879A-102

Query Match      73.6%; Score 16.2; DB 4; Length 571;
Best Local Similarity 85.7%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GTGATCTGCAAGATGAAC 21
Db  356 GTGACCTGGAAGAAGACTCA 376

RESULT 14
US-08-379-926A-7/c
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; Sequence 7, Application US/08379936A
; Patent No. 5783414
; GENERAL INFORMATION:
; APPLICANT: CARREZ, DIRK
; APPLICANT: ROOS, JOEL
; TITLE OF INVENTION: EXPRESSION SYSTEM, INTEGRATION
; TITLE OF INVENTION: VECTOR
; TITLE OF INVENTION: AND CELL TRANSFORMED BY THIS INTEGRATION VECTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESSEE: NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,926A
; FILING DATE: 27-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09400102
; FILING DATE: 28-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09400586
; FILING DATE: 17-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: BE 09500014
; FILING DATE: 09-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 3987-13-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2045 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-379-926A-7

Query Match 73.6%; Score 16.2; DB 1; Length 2045;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
Db 1377 GTATTCGCAGGATGAACCTCA 1357

RESULT 15
US-07-846-181-6/c
; Sequence 6, Application US/07846181
; Patent No. 5360732
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REV, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/846,181
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC204-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-846-181-6

Query Match 73.6%; Score 16.2; DB 1; Length 8533;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run On: December 5, 2002, 20:03:23 ; Search time 1.06939 Seconds
(without alignments)
8021.899 Million cell updates/sec

Title: US-09-856-937A-2

Perfect score: 22

Sequence: 1 gtgactctgaagatgaactcac 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	17.8	80.9	1855	9	US-10-000-512-5
2	17.8	80.9	3936	10	US-09-919-172-49
3	17.4	79.1	543	10	US-09-924-401-33
4	17.4	79.1	3103	9	US-09-925-302-85
5	17.4	79.1	5185	9	US-09-870-759-94
6	17.7	77.3	1850	10	US-09-822-830A-576
7	17.7	77.3	2570	12	US-10-036-342-17
8	17.7	77.3	2570	12	US-10-006-867-167
9	16.8	76.4	1503841	9	US-09-946-807-1
10	16.8	76.4	1503841	10	US-09-795-668-1
11	16.8	76.4	1503841	10	US-09-795-668-1
12	16.4	74.5	481	10	US-09-864-761-5696
13	16.2	73.6	302	10	US-09-560-863-683
14	16.2	73.6	571	10	US-09-884-441-102
15	15.8	71.8	470	10	US-09-864-761-1050
16	15.8	71.8	1004	9	US-09-938-842A-3644
17	15.8	71.8	1358	10	US-09-789-561-47
18	15.8	71.8	1493	9	US-09-992-598-134
19	15.8	71.8	1493	9	US-09-989-293A-134

C 20	15.8	71.8	1493	10	US-09-989-722-134	Sequence 134, App
C 21	15.8	71.8	1493	10	US-09-989-723-134	Sequence 134, App
C 22	15.8	71.8	1493	10	US-09-989-279-134	Sequence 134, App
C 23	15.8	71.8	1493	10	US-09-989-727-134	Sequence 134, App
C 24	15.8	71.8	1493	10	US-09-989-731-134	Sequence 134, App
C 25	15.8	71.8	1493	10	US-09-989-732-134	Sequence 134, App
C 26	15.8	71.8	1493	10	US-09-901-073-134	Sequence 134, App
C 27	15.8	71.8	1493	10	US-09-990-442-134	Sequence 134, App
C 28	15.8	71.8	1493	10	US-09-991-163-134	Sequence 134, App
C 29	15.8	71.8	1493	10	US-09-993-604-134	Sequence 134, App
C 30	15.8	71.8	1493	10	US-09-990-456-134	Sequence 134, App
C 31	15.8	71.8	1493	10	US-09-989-721-134	Sequence 134, App
C 32	15.8	71.8	1493	12	US-10-052-586-113	Sequence 113, App
C 33	15.8	71.8	1845	9	US-09-938-842A-2691	Sequence 2691, App
C 34	15.8	71.8	10096	10	US-09-960-253-163	Sequence 163, App
C 35	15.8	71.8	10190	10	US-09-864-864-292	Sequence 292, App
C 36	15.8	71.8	10211	10	US-09-954-456-1153	Sequence 1153, App
C 37	15.8	71.8	10211	10	US-09-967-768A-186	Sequence 186, App
C 38	15.8	71.8	55795	10	US-09-880-107-1543	Sequence 1543, App
C 39	15.6	70.9	933	10	US-09-815-242-6760	Sequence 6760, App
C 40	15.6	70.9	5233	10	US-09-070-927A-213	Sequence 213, App
C 41	15.6	70.9	167343	10	US-09-962-436-281	Sequence 281, App
C 42	15.6	70.9	167343	10	US-09-964-824A-273	Sequence 273, App
C 43	15.6	70.9	302250	10	US-09-962-832-154	Sequence 154, App
C 44	15.4	70.0	933	9	US-10-027-806-43	Sequence 43, App
C 45	15.4	70.0	32998	9	US-10-027-806-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-000-512-5
; Sequence 5, Application US/10000512
; Patent No. US20020164699A1
; GENERAL INFORMATION:
; APPLICANT: Shinketsu, Richard A
; APPLICANT: Fernandes, Elma
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAME
; FILE REFERENCE: 15966-556
; CURRENT APPLICATION NUMBER: US/10/000,512
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/619,252
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/167,785
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)..(1368)
US-10-000-512-5

Query Match 80.9% Score 17.8; DB 9; Length 1855;
Best Local Similarity 90.5%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTGATCTGCAAGATGAACCTCA 21
Db 790 GTGAAGTCAAGATGACCTCA 810
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|||||

RESULT 2
US-09-919-172-49
; Sequence 49, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.

;
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 49
; LENGTH: 3936
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1088524.8
; NAME/KEY: unsure
; LOCATION: 2060-2170, 3796, 3799, 3816
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-172-49

Query Match 80.9%; Score 17.8; DB 10; Length 3936;
Best Local Similarity 90.5%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACTCA 21
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DB 871 GTGAAGTCAAGATCACTCA 891

RESULT 3
US-09-924-401-33/C
; Sequence 33, Application US/09924401
; Patent No. US20020142957A1
; GENERAL INFORMATION:
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.550
; CURRENT APPLICATION NUMBER: US/09/924,401
; CURRENT FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 38, 451, 509, 537
; OTHER INFORMATION: n = A,T,C or G
US-09-924-401-33

Query Match 79.1%; Score 17.4; DB 10; Length 543;
Best Local Similarity 94.7%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACT 19
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DB 215 GTGATTTGCAAGATCACT 197

RESULT 4
US-09-925-302-85
; Sequence 85, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302

;
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 3103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (293)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-85

Query Match 79.1%; Score 17.4; DB 10; Length 3103;
Best Local Similarity 94.7%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATCACT 19
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DB 904 GTGATTTGCAAGATCACT 922

RESULT 5
US-09-870-759-94
; Sequence 94, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 5185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(4474)
; OTHER INFORMATION:
US-09-870-759-94

Query Match 79.1%; Score 17.4; DB 9; Length 5185;
Best Local Similarity 94.7%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ATCTGCAAGATCACTCAC 22
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DB 1556 ATCTGCAAGATCACTCAC 1574

RESULT 6
US-09-822-830A-576
; Sequence 576, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

; FILE REFERENCE: GIN 6402

; CURRENT APPLICATION NUMBER: US/09/822,830A

; CURRENT FILING DATE: 2001-03-29

; PRIOR APPLICATION NUMBER: 60/195,604

; PRIOR FILING DATE: 2000-04-06

; NUMBER OF SEQ ID NOS: 631

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 576

; LENGTH: 1850

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 2;

; OTHER INFORMATION: n=a,c,g, or t

US-09-822-830A-576

Query Match 77.3%; Score 17; DB 10; Length 1850;

Best Local Similarity 100.0%; Pred. No. 37;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GATCTCAAGATGAAGT 19

|||||

Db 617 GATCTCAAGATGAAGT 633

RESULT 7

US-10-036-342-17

; Sequence 17, Application US/10036342

; Patent No. US20020090681A1

; GENERAL INFORMATION:

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Watanabe, Collin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3030R1C5

; CURRENT APPLICATION NUMBER: US/10/036,342

; CURRENT FILING DATE: 2001-12-25

; PRIOR APPLICATION NUMBER: 60/085579

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: 60/112514

; PRIOR FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: 60/113300

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: 60/113430

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/113605

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/114140

; PRIOR FILING DATE: 1998-12-23

; PRIOR APPLICATION NUMBER: 60/115552

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/116843

; PRIOR FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: 60/125774

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/125778

; PRIOR FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/125826

; PRIOR FILING DATE: 1999-03-24

; PRIOR APPLICATION NUMBER: 60/127035

; PRIOR FILING DATE: 1999-03-31

; PRIOR APPLICATION NUMBER: 60/127706

; PRIOR FILING DATE: 1999-04-05

; PRIOR APPLICATION NUMBER: 60/129122

; PRIOR FILING DATE: 1999-04-13

; PRIOR APPLICATION NUMBER: 60/130359

; PRIOR FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: 60/131270

; PRIOR FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: 60/131272

; PRIOR FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: 60/131291

; PRIOR FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: 60/132371

; PRIOR FILING DATE: 1999-05-04

; PRIOR APPLICATION NUMBER: 60/132379

; PRIOR FILING DATE: 1999-05-04

; PRIOR APPLICATION NUMBER: 60/132383

; PRIOR FILING DATE: 1999-05-04

; PRIOR APPLICATION NUMBER: 60/135750

; PRIOR FILING DATE: 1999-05-25

; PRIOR APPLICATION NUMBER: 60/138166

; PRIOR FILING DATE: 1999-06-08

; PRIOR APPLICATION NUMBER: 60/144791

; PRIOR FILING DATE: 1999-07-20

; PRIOR APPLICATION NUMBER: 60/146970

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: 60/162506

; PRIOR FILING DATE: 1999-10-29

; PRIOR APPLICATION NUMBER: 09/311832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 09/380142

; PRIOR FILING DATE: 1999-08-25

; PRIOR APPLICATION NUMBER: 09/644848

; PRIOR FILING DATE: 2000-08-22

; PRIOR APPLICATION NUMBER: 09/747259

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: 09/816744

; PRIOR FILING DATE: 2001-03-22

; PRIOR APPLICATION NUMBER: 09/854208

; PRIOR FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 09/854280

; PRIOR FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 09/874503

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 09/869599

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: 09/908,827

; PRIOR FILING DATE: 2001-07-18

; PRIOR APPLICATION NUMBER: PCT/US99/10733

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: PCT/US99/28551

; PRIOR FILING DATE: 1999-12-02

; PRIOR APPLICATION NUMBER: PCT/US99/30720

; PRIOR FILING DATE: 1999-12-22

; PRIOR APPLICATION NUMBER: PCT/US00/05601

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: PCT/US00/05841

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: PCT/US00/14042

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: PCT/US00/15264

; PRIOR FILING DATE: 2000-06-02

; PRIOR APPLICATION NUMBER: PCT/US00/23522

; PRIOR FILING DATE: 2000-08-23

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: PCT/US00/32678

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: PCT/US00/34956

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: PCT/US01/06520

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: PCT/US01/17800

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; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/16692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 17
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-036-342-17

Query Match      77.3%; Score 17; DB 12; Length 2570;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 GATCTGCAAGATGAAC 19
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Db  1294 GATCTGCAAGATGAAC 1310

RESULT 8
US-10-006-867-167
; Sequence 167, Application US/10006867
; Patent No. US20020119130A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-11
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; PRIOR FILING DATE: 1998-06-16
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; PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/099815
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; PRIOR APPLICATION NUMBER: 60/100627
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
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; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102570
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 60/103449
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; PRIOR APPLICATION NUMBER: 60/103678
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; PRIOR FILING DATE: 1998-10-08
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; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
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; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106030
; PRIOR FILING DATE: 1998-10-28
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; PRIOR APPLICATION NUMBER: 60/108807
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/112419
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; PRIOR APPLICATION NUMBER: 60/112422
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; PRIOR APPLICATION NUMBER: 60/112854
; PRIOR FILING DATE: 1998-12-16
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; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113408
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; PRIOR FILING DATE: 1998-12-23
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; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114223
; PRIOR FILING DATE: 1998-12-30
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116527
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119525
; PRIOR FILING DATE: 1999-02-10
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; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/129674
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
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; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142

Query Match          77.3%; Score 17; DB 12; Length 2570;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GATCTGCAAGATGAAC 19
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Db      1294 GATCTGCAAGATGAAC 1310

RESULT 9
US-09-946-807-1/c
; Sequence 1, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946.807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795.668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: r-g or a
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: y-t/u or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: m-a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: k-g or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: s-g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: w-a or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: b-g or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
; OTHER INFORMATION: d-a or g or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1531)
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; OTHER INFORMATION: h=a or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v=a or g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1
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Query Match 76.4%; Score 16.8; DB 9; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 2 TGATCTGCAAGATGAACCTCA 21
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Db 1305659 TGATCTGCAAGATTAACCTCA 1305640
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US-09-795-668-1/c
; Sequence 1, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; CURRENT APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc_feature
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; OTHER INFORMATION: k=g or t/u
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; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: b=g or c or t/u
; NAME/KEY: misc_feature
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; OTHER INFORMATION: h=a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
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; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1
Query Match 76.4%; Score 16.8; DB 10; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGATCTGCAAGATGAACCTCA 21
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Db 1305659 TGATCTGCAAGATTAACCTCA 1305640
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RESULT 11
US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinhorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; CURRENT APPLICATION NUMBER: US/09/795,686
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r=g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y=t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m=a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k=g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s=g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w=a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b=g or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d=a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h=a or c or t/u
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; OTHER INFORMATION: v=a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1
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Query Match 76.4%; Score 16.8; DB 10; Length 1503841;
Best Local Similarity 90.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TGATCTGCAAGATGAACCTCA 21
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Db 1305659 TGATGTCGAAGATTAACCTCA 1305640

RESULT 12
US-09-864-761-5696/C
; Sequence 5696, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5696
; LENGTH: 481
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000055.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.1
US-09-864-761-5696

Query Match 74.5%; Score 16.4; DB 10; Length 481;

Best Local Similarity 94.4%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGATCTCGAAGATCAACT 19
Db 79 TGATCTCGAATATGAAC 62

RESULT 13
US-09-560-863-683
; Sequence 683, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020110809A1 Human Polynucleotides and the
; FILE REFERENCE: LEX-0018-USA
; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 683
; LENGTH: 302
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(302)
; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-683

Query Match 73.6%; Score 16.2; DB 10; Length 302;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATCTCGAAGATCAACTCA 21
Db 144 GTGGTCTCGAAGTGAACCTTA 164

RESULT 14
US-09-884-441-102
; Sequence 102, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSEQ for Windows version 3.0
; SEQ ID NO 102
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-884-441-102

Query Match 73.6%; Score 16.2; DB 10; Length 571;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTGATCTCGAAGATCAACTCA 21
Db 356 GTGACCTGGGAAGAAGAACTCA 376

RESULT 15
US-09-864-761-1050/c
; Sequence 1050, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1050
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008159.1
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; NAME/KEY: unsure
; LOCATION: 57
; NAME/KEY: unsure
; LOCATION: 256
US-09-864-761-1050

Query Match 71.8%; Score 15.8; DB 10; Length 470;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 465 GTGACCTGCAAGATGAATT 447
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Search completed: December 6, 2002, 00:17:39
Job time : 1463.07 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: December 5, 2002, 23:30:25 ; Search time 41.4471 Seconds
(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937A-3
Perfect score: 20
Sequence: 1 acaccagctctgatgtttca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: gb_htg.*
- 3: gb_in.*
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- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
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Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	20	100.0	199	9	AB030950
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C 4	20	100.0	705	6	ARI174443
C 5	20	100.0	1080	9	HUMTNFRA
C 6	20	100.0	1557	6	AX054825
C 7	20	100.0	1557	6	I36197
C 8	20	100.0	1641	6	I36196
C 9	20	100.0	2224	6	ARI152033
C 10	20	100.0	2253	6	A78517
C 11	20	100.0	2339	6	A26415
C 12	20	100.0	2394	9	HUMTNFRII
C 13	20	100.0	3380	11	G26865
C 14	20	100.0	3492	9	S63368
C 15	20	100.0	3683	6	AX333705
C 16	20	100.0	3683	6	AX348016
C 17	20	100.0	3683	6	AX348018
C 18	20	100.0	3683	6	AX348020
C 19	20	100.0	3683	9	HUMNFR
C 20	20	100.0	122105	2	AL355998
C 21	20	100.0	151498	9	AL357835
C 22	20	100.0	187877	2	AC023251
C 23	19	95.0	34	6	A20251
C 24	19	95.0	34	6	I43804
C 25	17.4	87.0	129418	2	AC015610
C 26	17.4	87.0	147571	2	AC080177
C 27	17.4	87.0	161739	9	AC105277
C 28	17.4	87.0	173088	2	AC109036
C 29	17.4	87.0	173858	2	AC068424
C 30	17.4	87.0	196229	2	AC107667
C 31	16.8	84.0	10387	1	AE013752
C 32	16.8	84.0	88203	5	AC097628
C 33	16.8	84.0	89044	2	AC022633
C 34	16.8	84.0	110188	2	AC105877
C 35	16.8	84.0	127422	8	OSJN00109
C 36	16.8	84.0	135638	1	SYCSLRG
C 37	16.8	84.0	142902	2	AC118897
C 38	16.8	84.0	156284	2	AC102977
C 39	16.8	84.0	162336	9	AC021594
C 40	16.8	84.0	164732	2	AC118946
C 41	16.8	84.0	170803	2	AP001641
C 42	16.8	84.0	176525	2	AL845474
C 43	16.8	84.0	182334	2	AP004724
C 44	16.8	84.0	184510	2	AC079059
C 45	16.8	84.0	190066	9	AC010127

ALIGNMENTS

RESULT 1
HSTNFR2S05/c
LOCUS HSTNFR2S05 106 bp DNA linear PRI 31-JUL-1996
DEFINITION Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 5.
ACCESSION U52160
VERSION U52160.1 GI:1469534
KEYWORDS 5 of 10
SEGMENT Homo sapiens.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 106)
AUTHORS Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
LePaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and

Brodeur, G.M.
 TITLE Physical mapping and genomic structure of the human TNFR2 gene
 JOURNAL Genomics 35 (1), 94-100 (1996)
 MEDLINE 96299745
 PUBMED 8661109
 REFERENCE 2 (bases 1 to 106)
 AUTHORS Beltinger, C.P., White, P.S., Maris, J.M., Sulman, E.P., Jensen, S.J., LePaslier, D., Stallard, B.J., Goeddel, D.V., deSauvage, F.J. and Brodeur, G.M.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-1996) Christian P. Beltinger, Division of Oncology, ARC Rm. 902 D, Children's Hospital of Philadelphia, 324 South 34th Street, Philadelphia, PA 19104-4318, USA
 FEATURES Location/Qualifiers
 Source 1..106
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="1"
 /map="1p36.2"
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 7..106
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 101..>106
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 /number=5
 26 a 31 c 28 g 21 t

FEATURES

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 7..106
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 26 a 31 c 28 g 21 t

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 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACACCGTCTGATGTTTCA 20
 |||||
 DB 30 ACACACCGTCTGATGTTTCA 11

RESULT 2
 AB030950/c
 LOCUS AB030950 Homo sapiens TNFR2 gene for tumor necrosis factor receptor 2,
 DEFINITION partial cds.
 ACCESSION AB030950
 VERSION AB030950.1 GI:6683131
 KEYWORDS tumor necrosis factor receptor 2; TNFR2.
 SOURCE Homo sapiens DNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Tsuchiya, N., Komata, T., Matsushita, M., Ohashi, J. and Tokunaga, K.
 TITLE New single nucleotide polymorphisms in the coding region of human TNFR2: association with systemic lupus erythematosus
 JOURNAL Genes Immun. 1 (8), 501-503 (2000)
 MEDLINE 21069356
 REFERENCE 2 (bases 1 to 199)

Komata, T., Tsuchiya, N. and Tokunaga, K.
 TITLE Direct Submission
 JOURNAL Submitted (09-AUG-1999) Tae Komata, University of Tokyo, Department of Human Genetics, Graduate School of Medicine, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan (E-mail: tae@n.u-tokyo.ac.jp, Tel: 81-3-5841-3693, Fax: 81-3-5802-8619)
 FEATURES Location/Qualifiers
 source 1..199
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 58..151
 /gene="TNFR2"
 <58..>151
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FEATURES

source 1..199
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 /db_xref="taxon:9606"
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 /gene="TNFR2"
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 /gene="TNFR2"

/codon_start=3
 /product="tumor necrosis factor receptor 2"
 /protein_id="BAA89053.1"
 /db_xref="GI:6683132"
 /translation="TETSDVVKPCAPGTFSTNTSSFDICRPHQ"
 58..151
 /gene="TNFR2"
 /number=5
 143
 /gene="TNFR2"
 /replace="c"
 40 a 51 c 62 g 46 t
 BASE COUNT 40 a 51 c 62 g 46 t
 ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 199;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACACCGTCTGATGTTTCA 20
 |||||
 DB 81 ACACACCGTCTGATGTTTCA 62

RESULT 3
 I36350/c
 LOCUS I36350 Sequence 12 from patent US 5606031.
 DEFINITION linear PAT 13-MAY-1997
 ACCESSION I36350
 VERSION I36350.1 GI:2086863
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 691)
 AUTHORS Lille, J., Kohno, T., Bonam, D. and Rosendahl, M. S.
 TITLE Production and purification of biologically active recombinant neurotrophic protein in bacteria
 JOURNAL Patent: US 5606031-A 12 25-FEB-1997;
 FEATURES Location/Qualifiers
 source 1..691
 /organism="unknown"
 BASE COUNT 160 a 198 c 190 g 143 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 691;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACACCGTCTGATGTTTCA 20
 |||||
 DB 553 ACACACCGTCTGATGTTTCA 534

RESULT 4
 AR174443/c
 LOCUS AR174443 Sequence 3 from patent US 6306820.
 DEFINITION linear PAT 17-DEC-2001
 ACCESSION AR174443
 VERSION AR174443.1 GI:17914763
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 705)
 AUTHORS Bendele, A. M., Sennello, R. M. and Edwards III, C. K.
 TITLE Combination therapy using a TNF binding protein for treating TNF-mediated diseases
 JOURNAL Patent: US 6306820-A 3 23-OCT-2001;
 FEATURES Location/Qualifiers
 source 1..705
 /organism="unknown"
 BASE COUNT 150 a 244 c 196 g 115 t
 ORIGIN


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Query Match      100.0%; Score 20; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACACCACGCTCTGATGTTTCA 20
    |||||||
Db 415 ACACCACGCTCTGATGTTTCA 396

RESULT 5
HUMTNFRA/c
LOCUS      HUMTNFRA      1080 bp      mRNA      linear      PRI 07-MAR-1995
DEFINITION Human tumor necrosis factor receptor protein (TNFR) mRNA, 3' end.
ACCESSION  M35857
VERSION     M35857.1 GI:339751
KEYWORDS   tumor necrosis factor receptor protein.
SOURCE     human parental B-cell UC/HeLa 2-5 cell line, cDNA to mRNA, clone 16.

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1080)
AUTHORS    Heller, R.A., Song, K., Onasch, M.A., Fischer, W.H., Chang, D. and Ringold, G.M.
TITLE      Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 87 (16), 6151-6155 (1990)
MEDLINE    90349572
PUBMED     2166946
COMMENT    Draft entry and computer-readable sequence for [1] kindly submitted by R.A.Heller, 29-JUN-1990.

FEATURES   source
            Location/Qualifiers
            1..1080
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /map="12p13"
            /clone="j16"
            /cell_line="UC/HeLa2-5"
            /cell_type="B-cell"
            /dev_stage="parent"
            1..1080
            /gene="TNFR1"
            <1..1041
            /gene="TNFR1"
            /note="tumor necrosis factor receptor protein (TNFR)"
            /codon_start=1
            /protein_id="AAA63262.1"
            /db_xref="GI:339752"
            /db_xref="GDB:G00-125-913"
            /translation="RICTCRPGWCYCALSKQEGRLCAPLPCRCRPGFGVARPGTETS DV
            VCKPCAPGTFSTSTSDICRPHQICNVVAIPGNASRDVACTSTSPTRSMAPGAVHLP
            QVTRSRQHTPTPEPSTAPSTFLLPMGPSPPAEGTGDFALPVLGVGTALGLLI
            IGVNVCVIMTVKKKPLCLOREAKYHPILADKARGTQGEQOHLITAPSSSSSSLES
            SASALDRAPTRNQAPQVEASGAGEARTKSDSDSPGGHGTVQNVNVCVSSS
            DHSSQSSQASSTMGDTDSSPESPKDEQVPFSECAFRSQLETPTLLGSTEKPL
            PLGVDPAGMKPS"
BASE COUNT    226 a 351 c 327 g 176 t
ORIGIN
Query Match      100.0%; Score 20; DB 9; Length 1080;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACACCACGCTCTGATGTTTCA 20
    |||||||
Db 136 ACACCACGCTCTGATGTTTCA 117

RESULT 6
AX054825/c
LOCUS      AX054825      1557 bp      DNA      linear      PAT 13-JAN-2001
DEFINITION Sequence 2 from Patent WO0073481.

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ACCESSION  AX054825
VERSION     AX054825.1 GI:12228270
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1557)
AUTHORS    Burstein, H. and Stepan, A.M.
TITLE      Methods and compositions for lowering the level of tumor necrosis factor (tnf) in tnfr-associated disorders
JOURNAL    Patent: WO 0073481-A 2 07-DEC-2000;
            TARGETED GENETICS CORPORATION (US)
FEATURES   source
            Location/Qualifiers
            1..1557
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            <1..1557
            /note="unnamed protein product"
            /codon_start=1
            /protein_id="CAC21968.1"
            /db_xref="GI:12228271"
            /translation="ARQAAWREGAGLRGREGARAGGNRTPTPASMAPVAVVAALAVGLE
            LWAAAHALPAQVAFTPYAPBPGNCRRLREYDOTAOMCCSKCSPGOHAKVCTKTSDT
            VCDSCEDSTYTLQNNWYPELSCGSRSSQVETQACTREQNRNICTCRPGWYCALSKQ
            EGCRLCAPLRKRCRPGFGVARPGTETS DVCKPCAPGTFSTSTSDICRPHQICNVVA
            IPGNASMDAVCTSTSPTRSMAPGAVHLPQVTRSRQHTPTPEPSTAPSTFLLPMGP
            SPPAEGTGDEPKSCDKTHCTPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
            VDVSHEDEPVKFNMYVDGVGVHNAKTKPREEOYNSTYRVSVLTVLHODMLNKDKYKC
            KVSNKALPAPMOKTISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKCKGKFPYPRITAV
            EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNFVSCSVMEALHNHTT
            QKSLSLSPGK"
BASE COUNT    345 a 526 c 445 g 241 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 1557;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACACCACGCTCTGATGTTTCA 20
    |||||||
Db 568 ACACCACGCTCTGATGTTTCA 549

RESULT 7
I36197/c
LOCUS      I36197      1557 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 3 from patent US 5605690.
ACCESSION  I36197
VERSION     I36197.1 GI:2086710
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
            1 (bases 1 to 1557)
            Jacobus, C.A. and Smith, C.A.
            Methods of lowering active TNF-.alpha. levels in mammals using
            tumor necrosis factor receptor
            Patent: US 5605690-A 3 25-FEB-1997;
FEATURES   source
            Location/Qualifiers
            1..1557
            /organism="unknown"
BASE COUNT    345 a 526 c 445 g 241 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 1557;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACACCACGCTCTGATGTTTCA 20
    |||||||
Db 568 ACACCACGCTCTGATGTTTCA 549

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RESULT 8
I36196/c
LOCUS       I36196               1641 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION   Sequence 1 from patent US 5605690.
ACCESSION    I36196
VERSION      I36196.1 GI:2086709
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 1641)
AUTHORS     Jacobs,C.A. and Smith,C.A.
TITLE       Methods of lowering active TNF- $\alpha$  levels in mammals using
            tumor necrosis factor receptor
JOURNAL      Patent: US 5605690-A 1 25-FEB-1997;
FEATURES     Location/Qualifiers
             source
             1..1641
             /organism="unknown"
BASE COUNT   328 a 544 c 502 g 267 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 1641;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACCACGCTCGATGTTTCA 20
|||||
Db 568 ACACCACGCTCGATGTTTCA 549

RESULT 9
ARI52033/c
LOCUS       ARI52033             2224 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION   Sequence 2 from patent US 6232446.
ACCESSION    ARI52033
VERSION      ARI52033.1 GI:15118083
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 2224)
AUTHORS     Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
TITLE       TNF ligands
JOURNAL      Patent: US 6232446-A 2 15-MAY-2001;
FEATURES     Location/Qualifiers
             source
             1..2224
             /organism="unknown"
BASE COUNT     435 a 598 c 689 g 402 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2224;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACCACGCTCGATGTTTCA 20
|||||
Db 570 ACACCACGCTCGATGTTTCA 551

RESULT 10
A78517/c
LOCUS       A78517             2253 bp      DNA      linear      PAT 19-OCT-1999
DEFINITION   Sequence 1 from Patent EP0585939.
ACCESSION    A78517
VERSION      A78517.1 GI:6090179
KEYWORDS     .
SOURCE       unidentified.
ORGANISM     unidentified.
REFERENCE    1 (bases 1 to 2253)
AUTHORS     Mett,I. and Wallach,D.
TITLE       TNF LIGANDS
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JOURNAL      Patent: BP 0585939-A 1 09-MAR-1994;
FEATURES     YEDA RES & DEV (IL)
             source
             1..2253
             /organism="unidentified"
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             /translation="MAPVAVMAALAVGLLWAAHALPAQVAFTPYAPEPGSTGRLE
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             CKPCARGTFSNNTSSDIDICRPHQICNVVAIPGNASNDVCTSTSPTRSMAPGAVHLPQ
             PYSTRSQHTQPTPEPSTAPSTFLLPMGSPPAEGSTGDFALPGLVIGVVTALGLLI
             GYVNCVIMTQVRKKPLCLQREAKVPHLPADKARGTQGPQQHLLITAPSSSSSLESS
             ASALDRRAPTRNOPQAGVEASGAGEARASTGSDSPGSGHTQVNTVCIVNVCSSD
             HSSQSSQASSTMGDTSSPSEPKDEQVFSKECAFRSQLETPETLLGSTEKPLP
             LGVPDAGMKPS"
BASE COUNT     440 a 709 c 698 g 406 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2253;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACACCACGCTCGATGTTTCA 20
|||||
Db 570 ACACCACGCTCGATGTTTCA 551

RESULT 11
A26415/c
LOCUS       A26415             2339 bp      DNA      linear      PAT 26-APR-1995
DEFINITION   CDNA fragment for (75kd TNF-BP) tumor necrosis factor binding
ACCESSION    A26415
VERSION      A26415.1 GI:904970
KEYWORDS     .
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
REFERENCE    1 (bases 1 to 2339)
AUTHORS     Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
            Schlaeger,E.J.
TITLE       TNF-binding proteins
JOURNAL      Patent: EP 0417563-A 27 20-MAR-1991;
            F. HOFFMANN-LA ROCHE AG
FEATURES     Location/Qualifiers
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             1..2339
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             /product="75kd TNF-BP"
             /protein_id="CAA01806.1"
             /db_xref="GI:904971"
             /translation="SDSVCDSCDSTVTOLMNNVPECLSGSRCSDDOVTQACTPEQ
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             PEPSTAPSTFLLPMGSPPAEGSTGDFALPGLVIGVVTALGLLIIGVYVNCVIMTQV
             KKPLCLQREAKVPHLPADKARGTQGPQQHLLITAPSSSSSLESSSALDRRAPTRN
             QPQAPGVEASGAGEARASTGSDSPGSGHTQVNTVCIVNVCSSDSSQSSQAS
             TMGDTSSPSEPKDEQVFSKECAFRSQLETPETLLGSTEKPLPVGPDAGMKPS"
BASE COUNT     494 a 720 c 685 g 440 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 2339;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACACACGCTCTGATGTTTCA 20
LOCUS
Db 271 ACACACGCTCTGATGTTTCA 252

RESULT 12
HUMTNFR1I/c
LOCUS
DEFINITION
Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.

ACCESSION
M55994 M38549
VERSION
M55994.1 GI:339757
KEYWORDS
glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.

SOURCE
Human histiocytic lymphoma cell line U937, cDNA to mRNA.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 2394)
AUTHORS
Kohn, T., Brewer, M.T., Baker, S.L., Schwartz, P.E., King, M.W., Hale, K.K., Squires, C.H., Thompson, R.C. and Vannice, J.L.
TITLE
A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)
MEDLINE
91045991
PubMed
2172983

FEATURES
source
1..2394
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/cell_type="histiocytic lymphoma"
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93..1478
/gene="TNFR1I"
/note="603..611 and 669..677 glycosylation site; 861..947 transmembrane domain; 948..1478 cytoplasmic domain; 159,,860 extracellular domain"
/codon_start=1
/evidence=experimental
/product="tumor necrosis factor receptor"
/protein_id="AAA36755.1"
/db_xref="GI:339758"
/translation="MAPVAVWAALAVGLLEWAAHALPAQVAFPPYAPFGSTCLRLRE YDQTAQMCSCSPQGHAKVFCSTKSDTVCDSCEDSTYQLNWNWPECLSGSRCS DQVETACTREQNRITCRPGWYKALSKQEGRLCAPLRKCRPGVARGPTSDV CKECAPGTSNTSSDIDICRHOICNVVAIPGNASDAVCTSTPTSRNAPGAVHLPQ PVSTRSQHTOPTPEPTSTFLLPMGPSPPAEGSTGDFALPVGLIVGVTALGLLII GVNCVIMTOVKKKPLCLQREAKVPHLPADKARGTGQPEQQHLLITPSSSSLESS ASALDRAPTRNQPQAPGVASGAGARASTSSDSSPGHGTVQNVTCIVNVCSSD HSSQCSQASSTMGDTSSPSPEKQVFPFSEKAFRSQLETPTLLGSTEERPLP LGVPDAGMKPS"
93..158
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/gene="TNFR1I"
/note="putative"
159..1475
mat_peptide
/gene="TNFR1I"
/product="tumor necrosis factor receptor"
/note="putative"
BASE COUNT 484 a 743 c 739 g 428 t

Query Match 100.0%; Score 20; DB 9; Length 2394;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACACGCTCTGATGTTTCA 20
LOCUS
Db 573 ACACACGCTCTGATGTTTCA 554

RESULT 13
G26865/c
LOCUS
DEFINITION
human STS SHGC-31494, sequence tagged site.
ACCESSION
G26865
VERSION
G26865.1 GI:1375115
KEYWORDS
STS; STS sequence; primer; sequence tagged site.
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3380)
AUTHORS
Myers, R.M.
JOURNAL
Unpublished (1995)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CCCACCACTAGGACTCTGA
Primer B: CACAGAGAGTCAGGACTTGC
STS size: 201
PCR Profile:
Initial Incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3
Prepared with primer pairs provided by Sandoz, derived from M32315
-- Washington University/Merck EST sequence.
FEATURES
source
Location/Qualifiers
1..3380
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/db_xref="taxon:9606"
/map="1"
STS
primer_bind 1561..1761
primer_bind 1561..1580
complement(1741..1761)
BASE COUNT 703 a 1029 c 1004 g 644 t
ORIGIN
Query Match 100.0%; Score 20; DB 11; Length 3380;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACACGCTCTGATGTTTCA 20
LOCUS
Db 570 ACACACGCTCTGATGTTTCA 551

RESULT 14
S63368/c
LOCUS
S63368
3492 bp mRNA linear PRI 06-MAR-2001

DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, partial cds.
ACCESSION S63368
VERSION S63368.1 GI:235648
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3492)
AUTHORS Dembic, Z., Loetscher, H., Gubler, U., Pan, Y. C., Lahm, H. W., Gentz, R.,
Brockhaus, M. and Lesslauer, W.
TITLE Two human TNF receptors have similar extracellular, but distinct
intracellular, domain sequences
JOURNAL Cytokine 2 (4), 231-237 (1990)
MEDLINE 91370690
PUBMED 1966549
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibs63368] from the original journal article.
This sequence comes from Figure 1.
FEATURES
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 373 ACACCACGCTGATGTTTCA 354
RESULT 15
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LOCUS AX333705 3683 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 4214 from Patent WO0194629.
ACCESSION AX333705
VERSION AX333705.1 GI:18124424
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 4214 13-DEC-2001;
Avalon Pharmaceuticals (US)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 781 a 1098 c 1086 g 718 t

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 570 ACACCACGCTGATGTTTCA 551
Search completed: December 6, 2002, 03:55:04
Job time : 56.6471 secs

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 : Search time 4.80891 Seconds
(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937A-3

Perfect score: 20

Sequence: 1 acaccacgtctgatgtttca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	21	AAA49209
2	20	100.0	20	21	AAA48203
3	20	100.0	691	16	AAT05443
4	20	100.0	705	19	AAV41549
5	20	100.0	705	19	AAV19802
6	20	100.0	705	20	AAV81733
7	20	100.0	705	21	AAZ45759
8	20	100.0	705	21	AAZ45760
9	20	100.0	705	21	AAZ45761
10	20	100.0	705	21	AAZ45762
11	20	100.0	705	21	AAZ45763
12	20	100.0	705	21	AAZ45764
13	20	100.0	705	21	AAZ45765
14	20	100.0	705	21	AAZ45766
15	20	100.0	705	21	AAZ45767
16	20	100.0	705	21	AAZ45768
17	20	100.0	705	21	AAZ45769
18	20	100.0	705	21	AAZ45770
19	20	100.0	705	21	AAZ45771
20	20	100.0	705	21	AAZ45772
21	20	100.0	705	21	AAZ45773
22	20	100.0	705	21	AAZ45774
23	20	100.0	705	21	AAZ45775
24	20	100.0	705	21	AAZ45776
25	20	100.0	705	21	AAZ45777
26	20	100.0	705	21	AAZ45778
27	20	100.0	705	21	AAZ45779
28	20	100.0	705	21	AAZ45780
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33	20	100.0	705	21	AAZ45785
34	20	100.0	705	21	AAZ45786
35	20	100.0	705	21	AAZ45787
36	20	100.0	705	21	AAZ45788
37	20	100.0	705	21	AAZ45789
38	20	100.0	705	21	AAZ45790
39	20	100.0	705	21	AAZ45791
40	20	100.0	705	21	AAZ45792
41	20	100.0	705	21	AAZ45793
42	20	100.0	705	21	AAZ45794
43	20	100.0	705	21	AAZ45795
44	20	100.0	705	21	AAZ45796
45	20	100.0	705	21	AAZ45797

C 10	20	100.0	705	21	AAZ45762
C 11	20	100.0	1557	15	AAQ45225
C 12	20	100.0	1557	22	AAC90446
C 13	20	100.0	1640	12	AAQ10990
C 14	20	100.0	1641	14	AAQ49931
C 15	20	100.0	1641	15	AAQ45224
C 16	20	100.0	2224	16	AAQ89544
C 17	20	100.0	2339	12	AAQ10956
C 18	20	100.0	2339	22	AAH48860
C 19	20	100.0	2339	22	AAQ10907
C 20	20	100.0	2393	12	AAC83951
C 21	20	100.0	2394	22	AAC83951
C 22	20	100.0	3683	24	ABK83997
C 23	20	100.0	3683	24	ABL65877
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C 25	20	100.0	3683	24	ABK33466
C 26	20	100.0	3683	24	ABK33467
C 27	19	95.0	34	13	AAQ24451
C 28	15.8	79.0	306	24	ABK76582
C 29	15.8	79.0	474	22	ABA52330
C 30	15.8	79.0	474	22	ABA22125
C 31	15.8	79.0	474	22	AAK00602
C 32	15.8	79.0	474	22	AAK26052
C 33	15.8	79.0	474	22	AAI10680
C 34	15.8	79.0	474	22	AAI13936
C 35	15.8	79.0	474	22	AAI00613
C 36	15.8	79.0	474	24	ABS00635
C 37	15.8	79.0	1712	20	AAZ27501
C 38	15.8	79.0	1712	22	AAZ09901
C 39	15.4	77.0	573	24	ABN63733
C 40	15.4	77.0	2382	23	ABL22962
C 41	15.4	77.0	3019	23	ABL09600
C 42	15.4	77.0	3115	22	AAH48125
C 43	15.4	77.0	12724	22	AAK88955
C 44	15.4	77.0	25785	22	AAK78465
C 45	15.2	76.0	416	23	ABV10946

ALIGNMENTS

RESULT 1
AAA49209
ID AAA49209 standard; DNA; 20 BP.
XX
AC AAA49209;
XX
DT 22-NOV-2000 (first entry)
XX
DE Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-CAR.
XX
KW Human; tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW osteoporosis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200032826-A1.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999; 99WO-US28403.
XX
PR 30-NOV-1998; 98US-0110268.
XX
{UYDR-} UNIV DREXEL.
XX
Spotilla LD;
DR WPI; 2000-412362/35.
XX
PT Identifying individuals at risk of developing osteoporosis comprises
PT assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
PT in a DNA sample from an individual -

XX Example 2; Page 11; 21pp; English.
 XX
 CC The present sequence is a PCR primer for the (CA)₁₆ repeat of intron 4 of
 CC the human tumour necrosis factor alpha receptor 2 (TNFR2) gene. It was
 CC thought that this intron might contain a polymorphism related to
 CC osteoporosis. However, it was shown that this was not so. However, exon
 CC 10 contains three polymorphic sites. By determining the genotype of an
 CC individual it is possible to identify those at risk of osteoporosis,
 CC which is characterised by low bone density and fragile bones, later in
 CC life. Those at greatest risk are those who possess allele 1, which is the
 CC rarest allele. This is particularly useful as many cases of osteoporosis
 CC go undetected at present.

XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACACGCTCTGATGTTTCA 20
 |||||
 DB 1 ACACACGCTCTGATGTTTCA 20

RESULT 2
 AAA48203
 ID AAA48203 standard; DNA; 20 BP.
 AC AAA48203;

XX 15-SEP-2000 (first entry)

XX Reverse PCR primer for detection of TNFRSF1B intron 4 polymorphism.

XX Tumour necrosis factor; TNF; TNF-R2; TNFRSF1B; PCR primer;
 KW tumour necrosis factor receptor superfamily member 1B; human;
 KW cardiovascular disease; coronary artery disease;
 KW non-insulin dependent diabetes mellitus; neuropathy in NIDDM;
 KW essential hypertension; hyperlipidemia; diabetic neuropathy;
 KW vasoprotective; antihypertensive; lipid-lowering;
 KW chromosome lp36.2; D1S2834; ss.

XX Homo sapiens.

OS W0200031293-A1.

XX 02-JUN-2000.

XX 25-NOV-1999; 99WO-AU01050.

XX 25-NOV-1998; 98AU-0007323.

XX (UNSY) UNIV SYDNEY.

XX Morris BJ;

XX WPI; 2000-400096/34.

XX Method for diagnosing a predisposition to a complex polygenic disease
 PT e.g. coronary heart disease, hyperlipidemia and non-insulin-dependent
 PT diabetes mellitus comprises assaying chromosome 1 for a genetic marker

XX Claim 30; Page 3; 50pp; English.

XX A novel method for determining a predisposition in a subject to a
 CC complex polygenic disease involves assaying chromosome 1 for a
 CC genetic marker indicative of a predisposition to the disease. This
 CC method may be used for determining predisposition to cardiovascular
 CC disease, coronary artery disease, non-insulin dependent diabetes
 CC mellitus, neuropathy in NIDDM, essential hypertension, hyperlipidemia
 CC and diabetic neuropathy. The method can be used for testing an

CC individual with a family history or in the early stages of a complex
 CC polygenic disease to ascertain the chance of developing hypertension,
 CC neuropathy or lipid disturbances such as high total cholesterol, high
 CC low density lipoprotein cholesterol, abnormal apolipoprotein AI and
 CC abnormal glycosylated haemoglobin. Once a complex polygenic disease
 CC disposition has been identified the subject can be treated to prevent
 CC or reduce the disease or delay its onset. The genetic marker used
 CC in the method is D1S2834 and includes a CA repeat region in intron
 CC 4 of the tumour necrosis factor receptor superfamily member 1B
 CC (TNFRSF1B) gene. The marker is located at chromosome lp36.2. The
 CC present sequence is the reverse PCR primer used for detection of
 CC the TNFRSF1B intron 4 polymorphism.

XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.58;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACACGCTCTGATGTTTCA 20
 |||||
 DB 1 ACACACGCTCTGATGTTTCA 20

RESULT 3
 AAT05443/c
 ID AAT05443 standard; DNA; 691 BP.
 AC AAT05443;

XX 10-FEB-1996 (first entry)

XX BamTP delta53 nerve growth factor sequence.

XX Nerve growth factor; neurotrophic factor; therapeutic;
 KW protein refolding; NGF; plasmid pT3XI-2; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FT 136..687
 CDS /*tag= a
 FT /*note= "NGF"

XX W09530686-A1.

XX 16-NOV-1995.

XX 02-MAY-1995; 95WO-US05423.

XX 27-JUN-1994; 94US-0266080.

XX 09-MAY-1994; 94US-0240122.

XX (SYNT) SYNTX-SYNERGEN NEUROSCIENCE JOINT VENTU.

XX Bonam D, Kohno T, Lile J, Rosendahl MS;

XX WPI; 1995-404080/51.

XX P-PSDB; AAR77421.

XX Process for bacterial expression of recombinant neurotrophic factor
 PT - useful for promoting the survival and maintaining phenotypic
 PT differentiation of nerve and glial cells.

XX Example 1; Page 36-37; 57pp; English.

XX The synthetic nerve growth factor (NGF) gene isolated from Bam TP
 CC delta 53 plasmid pT3XI-2 is designed to optimize codons for
 CC expression in Escherichia coli as well as create unique sites for
 CC subsequent cloning steps. The recombinant protein is solubilized
 CC and sulfonylated and allowed to refold in the presence of PEG and
 CC urea. Biologically active NGF, used for promoting the survival of
 CC and maintaining the phenotypic differentiation of nerve and glial

CC cells, is isolated and purified. This method breaks incorrectly
 CC formed disulphide bonds and allows refolding of the factor into
 CC the correct tertiary structure required for maximum yield of full
 CC active protein.
 XX

SQ Sequence 691 BP; 160 A; 198 C; 190 G; 143 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 691;

Best Local Similarity 100.0%; Pred. No. 0.88; Length 691;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCAGCTCTGATGTTTCA 20
 ID AAV41549 standard; cDNA: 705 BP.
 XX AAV41549;
 AC AAV41549;
 XX 28-SEP-1998 (first entry)
 DT Human soluble tumour necrosis factor receptor type II.
 XX Human soluble tumour necrosis factor receptor type II.
 DE Human soluble tumour necrosis factor receptor type II;
 KW tumour necrosis factor; TNF; TNF receptor type II;
 KW inflammatory disease; leukaemia; TNF binding protein;
 KW anti-inflammatory drug; methotrexate; ss.
 XX Homo sapiens.
 XX

RESULT 4

AAV41549/C
 ID AAV41549 standard; cDNA: 705 BP.
 XX AAV41549;
 AC AAV41549;
 XX 28-SEP-1998 (first entry)
 DT Human soluble tumour necrosis factor receptor type II.
 XX Human soluble tumour necrosis factor receptor type II;
 KW tumour necrosis factor; TNF; TNF receptor type II;
 KW inflammatory disease; leukaemia; TNF binding protein;
 KW anti-inflammatory drug; methotrexate; ss.
 XX Homo sapiens.
 XX

Key Location/Qualifiers
 CDS 1..483
 FT /*tag a
 FT /product= "human soluble TNF receptor type II"
 FT
 XX WO9824463-A2.
 XX 11-JUN-1998.
 XX 08-DEC-1997; 97WO-US22733.
 XX 09-JUL-1997; 97US-0052023.
 XX 06-DEC-1996; 96US-0032587.
 XX 23-JAN-1997; 97US-0036355.
 XX 07-FEB-1997; 97US-0039315.
 XX (AMGE-) AMGEN INC.
 XX Benidele AM, Edwards CK, Sennello RM;
 XX WPI: 1998-333039/29.
 XX P-PSDB; AAW59665.
 XX Treatment of acute or chronic inflammatory disease, e.g. leukaemia -
 PT by administering tumour necrosis factor binding protein and at least
 PT one additional anti-inflammatory drug, e.g. methotrexate
 XX Disclosure; Fig 2; 104pp; English.
 XX This is the nucleotide sequence of the human tumour necrosis factor
 CC receptor type II, used in the method of the invention involving the
 CC treatment of acute or chronic inflammatory disease such as leukaemia
 CC by administering tumour necrosis factor binding protein and at least
 CC one additional anti-inflammatory drug, e.g. methotrexate.
 XX
 SQ Sequence 705 BP; 150 A; 244 C; 196 G; 115 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 705;

Best Local Similarity 100.0%; Pred. No. 0.88;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCAGCTCTGATGTTTCA 20
 ID AAV19802 standard; cDNA: 705 BP.
 XX AAV19802;
 AC AAV19802;
 XX 29-JUN-1998 (first entry)
 DT Tumour necrosis factor inhibitor coding sequence.
 XX Soluble tumour necrosis factor receptor; stnfr; TNF-mediated disease;
 KW tumour necrosis factor binding protein; autoimmune disease; arthritis;
 KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;
 KW tumour necrosis factor inhibitor; Alzheimer's disease; TNBP; ss.
 XX Homo sapiens.
 XX WO9801555-A2.
 XX 15-JAN-1998.
 XX 09-JUL-1997; 97WO-US12244.
 XX 04-MAR-1997; 97US-0039792.
 XX 09-JUL-1996; 96US-0021443.
 XX 06-DEC-1996; 96US-0032534.
 XX 23-JAN-1997; 97US-0037737.
 XX 07-FEB-1997; 97US-0039314.
 XX (AMGE-) AMGEN INC.
 XX Edwards CK, Fisher EF, Kieft GL;
 XX WPI: 1998-101052/09.
 XX P-PSDB; AAW52270.
 XX Truncated and soluble forms of tumour necrosis factor receptor -
 PT useful for treating diseases involving factor, e.g. arthritis and
 PT adult respiratory distress syndrome
 XX Claim 3; Fig 8; 205pp; English.
 XX This sequence encodes human tumour necrosis factor inhibitor. The protein
 CC was used to make the truncated soluble tumour necrosis factor receptor
 CC (stnfr) proteins of the invention. The truncated stnfr proteins and
 CC tumour necrosis factor binding proteins (TNBP) are used to treat any
 CC TNF-mediated disease, e.g. arthritis, adult respiratory distress
 CC syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft
 CC rejection, Alzheimer's disease and other autoimmune diseases. Cells
 CC transformed with a vector containing DNA encoding the protein may be used
 CC for production of recombinant stnfr, which may also be used for measuring
 CC the amount of stnfr in samples and to raise antibodies against stnfr.
 CC TNBP may also be used in preparation of therapeutic compositions for
 CC treating the above diseases. The stnfr proteins are well suited to large
 CC scale production (since they lack the deamidation site in region 111-126,
 CC so are more stable in vivo); contain fewer disulphide bonds and fewer
 CC epitopes, making them less antigenic than full-length proteins.
 XX
 SQ Sequence 705 BP; 150 A; 244 C; 196 G; 115 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 705;

Best Local Similarity 100.0%; Pred. No. 0.88;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCAGCTCTGATGTTTCA 20
 ID AAV19802 standard; cDNA: 705 BP.
 XX AAV19802;
 AC AAV19802;
 XX 29-JUN-1998 (first entry)
 DT Tumour necrosis factor inhibitor coding sequence.
 XX Soluble tumour necrosis factor receptor; stnfr; TNF-mediated disease;
 KW tumour necrosis factor binding protein; autoimmune disease; arthritis;
 KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;
 KW tumour necrosis factor inhibitor; Alzheimer's disease; TNBP; ss.
 XX Homo sapiens.
 XX WO9801555-A2.
 XX 15-JAN-1998.
 XX 09-JUL-1997; 97WO-US12244.
 XX 04-MAR-1997; 97US-0039792.
 XX 09-JUL-1996; 96US-0021443.
 XX 06-DEC-1996; 96US-0032534.
 XX 23-JAN-1997; 97US-0037737.
 XX 07-FEB-1997; 97US-0039314.
 XX (AMGE-) AMGEN INC.
 XX Edwards CK, Fisher EF, Kieft GL;
 XX WPI: 1998-101052/09.
 XX P-PSDB; AAW52270.
 XX Truncated and soluble forms of tumour necrosis factor receptor -
 PT useful for treating diseases involving factor, e.g. arthritis and
 PT adult respiratory distress syndrome
 XX Claim 3; Fig 8; 205pp; English.
 XX This sequence encodes human tumour necrosis factor inhibitor. The protein
 CC was used to make the truncated soluble tumour necrosis factor receptor
 CC (stnfr) proteins of the invention. The truncated stnfr proteins and
 CC tumour necrosis factor binding proteins (TNBP) are used to treat any
 CC TNF-mediated disease, e.g. arthritis, adult respiratory distress
 CC syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft
 CC rejection, Alzheimer's disease and other autoimmune diseases. Cells
 CC transformed with a vector containing DNA encoding the protein may be used
 CC for production of recombinant stnfr, which may also be used for measuring
 CC the amount of stnfr in samples and to raise antibodies against stnfr.
 CC TNBP may also be used in preparation of therapeutic compositions for
 CC treating the above diseases. The stnfr proteins are well suited to large
 CC scale production (since they lack the deamidation site in region 111-126,
 CC so are more stable in vivo); contain fewer disulphide bonds and fewer
 CC epitopes, making them less antigenic than full-length proteins.
 XX
 SQ Sequence 705 BP; 150 A; 244 C; 196 G; 115 T; 0 other;

```

RESULT 6
AAV81733/c
ID AAV81733 standard; cDNA; 705 BP.
XX
AC AAV81733;
XX
DT 04-MAR-1999 (first entry)
XX
DE Tumour necrosis inhibitor 40 kDa encoding cDNA.
XX
KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
KW inflammation; apoptosis; ss.
XX
OS Homo sapiens.
XX
PN WO9849305-A1.
XX
PD 05-NOV-1998.
XX
PF 29-APR-1998; 98WO-US08631.
XX
PR 01-MAY-1997; 97US-0850188.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boyle WJ, Wooden S;
XX
DR WPI: 1999-034661/03.
DR P-PSDB: AAW89234.
XX
PT New chimeric osteoprotegerin polypeptides - contain the
PT osteoprotegerin dimerisation domain and a heterologous sequence,
PT useful to treat TNF and TNFR-mediated disorders
XX
PS Disclosure; Fig 3; 92pp; English.
XX
CC The present invention describes a chimeric polypeptide (A1), comprising
CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous
CC amino acid sequence. Also described are: (1) a multimer polypeptide
CC comprising covalently associated A1 monomers; (2) an isolated nucleic
CC acid encoding A1; (3) an expression vector comprising the nucleic acid
CC sequence; and (4) a host cell transformed or transfected with the
CC expression vector so that the nucleic acid is expressible. The products
CC from the present invention are useful to treat a variety of disorders
CC including those related to receptor binding. Compositions comprising
CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras
CC are used to treat TNF and TNFR-mediated disorders such as inflammation,
CC autoimmune diseases and disorders related to excessive apoptosis. The
CC chimeras are also useful for detecting molecules which interact with
CC fused heterologous sequences to identify potential new receptors and
CC ligands. The present sequence encodes the TNF inhibitor 40 kDa protein.
XX
SQ Sequence 705 BP; 150 A; 244 C; 196 G; 115 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGTCGTGATGTTTCA 20
DB 415 ACACCACGTCGTGATGTTTCA 396

RESULT 7
AAZ45759/c
ID AAZ45759 standard; DNA; 705 BP.
XX
KW p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;

```

```

XX AAZ45759;
AC
XX 25-APR-2000 (first entry)
XX
DE DNA encoding a K108R mutant of soluble p75 TNF receptor.
XX
KW p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;
KW polyethylene glycol conjugation; PEG conjugation; protein activity; ss.
XX
OS Homo sapiens.
OS Synthetic.
PN WO9967291-A2.
XX
PD 29-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US13953.
XX
PR 22-JUN-1998; 98US-0102530.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Pettit DK;
XX
DR WPI: 2000-160577/14.
DR P-PSDB: AAY54440.
XX
PT Novel methods for site-specific protein modification by mutagenesis by
PT replacing polyethylene glycol reacting sites -
XX
PS Example 2; Page 28; 36pp; English.
XX
CC The present sequence encodes a N-terminal fragment of a mutant of
CC the soluble tumour necrosis factor (TNF) receptor, where the wild
CC type Lys residue at position 108 is replaced with Arg. Lys108 (and
CC Lys120) make contact between the p75 receptor and ligand. These
CC residues are also potential polyethylene glycol (PEG) conjugation
CC sites. The wild type p75 TNF receptor protein was mutated and conjugated
CC to PEG, using the method of the invention. The specification describes
CC a method for conjugating proteins with PEG to result in
CC PEG-conjugated proteins having little or no reduction in a desired
CC activity. Specifically, one or more amino acid residues that are
CC critical for protein bioactivity and which are capable of reacting
CC with PEG sites are deleted, prior to conjugation of the protein to PEG.
CC The methods provide PEG conjugated proteins that are more homogeneous
CC and present in higher yields. Conjugation does not take place at amino
CC acid residues that are critical to the proteins bioactivity, thus
CC maintaining the activity of the protein. The methods are used to
CC produce PEG conjugated proteins.
XX
SQ Sequence 705 BP; 150 A; 244 C; 195 G; 116 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGTCGTGATGTTTCA 20
DB 415 ACACCACGTCGTGATGTTTCA 396

RESULT 8
AAZ45760/c
ID AAZ45760 standard; DNA; 705 BP.
XX
AC AAZ45760;
XX
DT 25-APR-2000 (first entry)
XX
DE DNA encoding a K120R mutant of soluble p75 TNF receptor.
XX
KW p75 tumour necrosis factor receptor; mutant; PEG conjugated protein;

```


DR WPI: 2000-160577/14.
 DR P-PSDB; AAY54443.
 XX
 PT Novel methods for site-specific protein modification by mutagenesis by
 PT replacing polyethylene glycol reacting sites -
 XX
 PS Example 2; Page 34-35; 36pp; English.
 XX
 CC The present sequence encodes a N-terminal fragment of the soluble
 CC tumour necrosis factor (TNF) receptor. The wild type Lys residues at
 CC positions 108 and 120 are replaced with Arg (see AAY54441-42). Lys120
 CC and Lys108 make contact between the p75 receptor and ligand. These
 CC residues are also potential polyethylene glycol (PEG) conjugation
 CC sites. The wild type p75 TNF receptor protein was mutated and conjugated
 CC to PEG, using the method of the invention. The specification describes
 CC a method for conjugating proteins with PEG to result in
 CC PEG-conjugated proteins having little or no reduction in a desired
 CC activity. Specifically, one or more amino acid residues that are
 CC critical for protein bioactivity and which are capable of reacting
 CC with PEG sites are deleted, prior to conjugation of the protein to PEG.
 CC The methods provide PEG conjugated proteins that are more homogeneous
 CC and present in higher yields. Conjugation does not take place at amino
 CC acid residues that are critical to the proteins bioactivity, thus
 CC maintaining the activity of the protein. The methods are used to
 CC produce PEG conjugated proteins.
 XX
 SQ Sequence 705 BP; 151 A; 244 C; 194 G; 116 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 705;
 Best Local Similarity 100.0%; Pred. No. 0.88;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
 |||||
 DB 415 ACACCACGCTGATGTTTCA 396

RESULT 11
 ID AAQ45225/C
 XX AAQ45225 standard; cDNA; 1557 BP.
 AC AAQ45225;
 XX
 DT 07-OCT-1994 (first entry)
 DE
 DE TNFR/fc fusion protein.
 XX
 KW Tumour necrosis factor receptor; chimeric antibody molecule;
 KW Immunoglobulin; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 1..1554
 FT /*tag- a
 XX
 PN WO9406476-A.
 XX
 PD 31-MAR-1994.
 XX
 PF 14-SEP-1993; 93WO-US08666.
 XX
 PR 15-SEP-1992; 92US-0946236.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Jacobs CA, Smith CA;
 PI
 XX WPI: 1994-118172/14.
 DR P-PSDB; AAR51003.
 XX
 PT Treating TNF mediated inflammatory diseases with TNF antagonist -

PT esp. soluble form of TNF receptor, opt. as fusion protein with
 PT human immunoglobulin Fc region, esp. for treating arthritis
 XX
 PS Disclosure; Page 32-34; 47pp; English.
 XX
 CC AAQ45224 is cDNA from clone 1 of library WI-26 V44 of human fibroblast
 CC cell line WI-26 V44. The mature full-length TNFR1 is a glycoprotein
 CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
 CC TNFR1 was described in Smith et al., Science 248:1019,1990. Clone 1
 CC is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). A
 CC recombinant chimeric antibody may be produced having TNFR sequences
 CC substituted for the variable domains of either or both of the
 CC immunoglobulin molecule heavy and light chains and having
 CC unmodified constant region domains. A specific example of a TNFR/Fc
 CC fusion protein is given in AAQ45225/R51003. The rhu TNFR:Fc fusion
 CC gene was created by ligating the following fragments into a cloning
 CC vector: 1) an 867 bp Asp718-Pvu2 fragment from pCAV/NOT-TNFR (ATCC
 CC 68088) contg. the cDNA encoding the truncated TNFR. 2) a 700 bp
 CC Styl-SpeI fragment from plasmid pIXV498 coding for 232 AAs of the
 CC Fc portion of human IgG1. Plasmid pIXV498 is a yeast expression
 CC vector contg. the Fc fragment of human IgG1. 3) An oligo linker, to
 CC fuse the truncated TNFR with the human IgG1 Fc fragment. This
 CC linker was created by PCR using primer AAQ45226, which encodes the 3'
 CC end of the truncated TNF receptor and the 5' end of human IgG1 and
 CC primer AAQ45227, which is an antisense sequence encoding bps 257-237
 CC of human IgG1.
 XX
 SQ Sequence 1557 BP; 345 A; 524 C; 445 G; 243 T; 0 other;

Query Match 100.0%; Score 20; DB 15; Length 1557;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
 |||||
 DB 568 ACACCACGCTGATGTTTCA 549

RESULT 12
 AAC90446/C
 ID AAC90446 standard; cDNA; 1557 BP.
 XX
 AC AAC90446;
 XX
 DT 19-MAR-2001 (first entry)
 DE
 DE TNFR:Fc fusion protein coding sequence.
 XX
 KW Antinflammatory; antiarthritic; gene therapy; inflammatory disorder;
 KW Tumour Necrosis Factor receptor; TNFR; IgG1 Fc domain; asthma;
 KW rheumatoid arthritis; Crohn's disease; congestive heart failure; ss.
 XX
 OS Rattus sp.
 XX
 PN WO200073481-A1.
 XX
 PD 07-DEC-2000.
 XX
 XX 26-MAY-2000; 2000WO-US14586.
 PF
 XX 28-MAY-1999; 99US-0150688.
 PR
 XX (TARG-) TARGETED GENETICS CORP.
 PA
 XX Burstein H, Stepan AM;
 PI
 XX WPI: 2001-061552/07.
 DR P-PSDB; AAB50080.

Recombinant adeno-associated virus vector, useful for palliating tumor
 PT necrosis factor associated disorder, comprises polynucleotide which
 PT encodes fusion polypeptide comprising tumor necrosis factor receptor -

PS Example 1; Fig 2; 90pp; English.

XX The present invention relates to a recombinant adeno-associated virus
CC (rAAV) vector comprising a polynucleotide (the present sequence) which
CC encodes a fusion protein comprising an extracellular domain of Tumour
CC Necrosis Factor receptor (TNFR) and a constant domain (Fc) of IgG1
CC molecule. The vector of the present invention is useful for reducing TNF
CC levels, for reducing an inflammatory response which occurs in a
CC connective tissue and for palliating a TNF-associated disorder such as
CC inflammatory disorders e.g. rheumatoid arthritis, Crohn's disease, asthma
CC and congestive heart failure.

XX SQ Sequence 1557 BP; 345 A; 526 C; 445 G; 241 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 1557;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACCACGCTCGATGTTTCA 20

|||||

Db 568 ACACCACGCTCGATGTTTCA 549

RESULT 13

AAQ10990/c

ID AAQ10990 standard; cDNA to mRNA; 1640 BP.

XX AC AAQ10990;

DT 24-MAY-1991 (first entry)

XX Partial sequence of hTNF-R clone 1.

DE Tumour necrosis factor receptor; immune response; inflammation;
KW cachexia; septic shock; ss.

XX Homo sapiens.

Key Location/Qualifiers
FT CDS 88..1473

FT /*tag= a

FT mat_peptide 154..1470

FT /*tag= b

FT sig_peptide 88..153

FT /*tag= c

XX EP418014-A.

XX 20-MAR-1991.

XX 10-SEP-1990; 90EP-0309875.

XX 10-MAY-1990; 90US-0523635.

PR 11-SEP-1989; 89US-0405370.

PR 13-OCT-1989; 89US-0421417.

XX (IMMU-) IMMUNEX CORP.

XX Smith CA, Goodwin RG, Beckmann PW;

XX WPI: 1991-082230/12.

XX P-PSDB: AAR11141.

XX New tumour necrosis factor -alpha and -beta receptors - and DNA
PT encoding these used to regulate immune responses in treatment of
PT cachexia, septic shock or side-effects of cytokine therapy.

XX Claim 1; Fig 2; 41pp; English.

XX The sequence was obtd. from a clone isolated from library prepd.
CC from a human fibroblast cell line, WI-26 VA4 (ATCC CCL 95, 1).
CC The clone is deposited as Accession No. 68088 under the name
CC pCAV/NOT-TNF-R. The DNA can be truncatd to produce sequences which

CC express soluble receptor comprising residues 1-235, 1-185 or 1-163
CC of the protein.
CC See also AAQ10991.

XX SQ Sequence 1640 BP; 328 A; 543 C; 502 G; 267 T; 0 other;

Query Match 100.0%; Score 20; DB 12; Length 1640;

Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACACCACGCTCGATGTTTCA 20

|||||

Db 568 ACACCACGCTCGATGTTTCA 549

RESULT 14

AAQ49931/c

ID AAQ49931 standard; cDNA to mRNA; 1641 BP.

XX AC AAQ49931;

XX 29-APR-1994 (first entry)

XX TNF-R cDNA.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 88..1473

FT /*tag= a

FT sig_peptide 88..153

FT mat_peptide 154..1470

FT /*tag= c

XX WO9319777-A.

XX 14-OCT-1993.

XX 26-MAR-1993; 93WO-US02938.

XX 30-MAR-1992; 92US-0860710.

XX (IMMV) IMMUNEX CORP.

XX Smith CA;

XX WPI: 1993-336592/42.

XX P-PSDB: AAR42058.

XX New fusion protein tumour necrosis factor and human interleukin-1

XX receptor - useful in therapy, diagnosis and assays of e.g.

XX rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.

XX Disclosure; Fig 2; 85pp; English.

XX The sequences given in AAQ49931-32 encode human tumour necrosis factor

XX receptor (TNF-R) and the sequences in AAQ49933-34 encode human

XX interleukin-1 receptor (IL-1R). These sequences were used in the

XX production of a fusion protein which conformed to one of the

XX formulae:

XX TNF-R-linker-TNF-R-linker-IL-1R

XX IL-1R-linker-TNF-R-linker-TNF-R or

XX TNF-R-linker-TNF-R

XX The linker may comprise 5-100 amino acids selected from Gly, Asp,

CC Ser, Thr and Ala. These linkers separate the individual moieties
CC by such a distance that each component of the fusion protein is
CC capable of folding into the secondary or tertiary structure required
CC for its biological activity. These fusion proteins may be used in
CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC particularly in conditions in which both TNF and IL-1 play a causative
CC role. They may be used to treat cachexia, rheumatoid arthritis,
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC cerebral malaria, allograft and xenograft rejection in graft versus
CC host disease, sepsis, septic shock, inflammation, allergies and
CC autoimmune dysfunctions.

XX
SQ Sequence 1641 BP; 328 A; 544 C; 502 G; 267 T; 0 other;
Query Match 100.0%; Score 20; DB 14; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTCTGATGTTTCA 20
|||||
Db 568 ACACCACGCTCTGATGTTTCA 549

RESULT 15
AAQ45224/c
ID AAQ45224 standard; cDNA; 1641 BP.
AC AAQ45224;
XX
DT 07-OCT-1994 (first entry)
XX
DE Sequence encoding human tumour necrosis factor receptor type I
DE (TNFRI).
XX
KW Tumour necrosis factor receptor; type I; TNFRI; arthritis therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 154..1470
FT /*tag= a
FT sig_peptide 88..153
FT /*tag= b

XX W09406476-A.
XX
XX 31-MAR-1994.
XX
XX 14-SEP-1993; 93WO-US08666.
XX
XX 15-SEP-1992; 92US-0946236.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Jacobs CA, Smith CA;
XX
XX WPI; 1994-118172/14.
XX
XX P-PSDB; AAR51002.
XX
XX Treating TNF mediated inflammatory diseases with TNF antagonist -
XX esp. soluble form of TNF receptor, opt. as fusion protein with
XX human immunoglobulin Fc region, esp. for treating arthritis
XX
XX Disclosure: Page 28-30; 47pp; English.
XX
XX AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
XX cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein
XX having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
XX TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1
XX is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The
XX preferred TNFRs of the present invention are soluble forms of TNFRI
XX and TNFRII having at least 20 AAs. Soluble TNFR constructs are
XX devoid of a transmembrane region but retain the ability to bind TNF.

CC Examples of soluble TNFRs are huTNFRdelta235, huTNFRdelta185 and
CC huTNFRdelta163 which encode respectively AAs 1-235, 1-185 and 1-163
CC of AAR51002. An equivalent soluble TNFR is huTNFRdelta163 wherein x
CC is selected from any one of AAs 163-235 of AAR51002.
XX
SQ Sequence 1641 BP; 328 A; 526 C; 520 G; 267 T; 0 other;
Query Match 100.0%; Score 20; DB 15; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTCTGATGTTTCA 20
|||||
Db 568 ACACCACGCTCTGATGTTTCA 549

Search completed: December 5, 2002, 23:30:00
Job time : 8.80891 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 ; Search time 38.2783 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937A-3

Perfect score: 20
Sequence: 1 acaccacgtctgatgtttca 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	20	100.0	652	12	BF204631
c 5	20	100.0	741	12	BG828205
c 6	20	100.0	777	10	BE299738

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C	8	20	100.0	807	13	BI822108
C	9	20	100.0	982	12	BF310740
C	10	20	100.0	1177	12	BG109353
C	11	20	100.0	2291	11	BC011844
C	12	18	90.0	680	9	AJ272769
C	13	17.4	87.0	1097	14	BQ924155
C	14	17	85.0	301	17	AO816262
C	15	17	85.0	780	12	BF203997
C	16	16.8	84.0	220	9	AJ265128
C	17	16.8	84.0	323	9	AJ264082
C	18	16.8	84.0	335	9	AJ264081
C	19	16.8	84.0	391	9	AJ268690
C	20	16.8	84.0	405	9	AJ265129
C	21	16.8	84.0	406	9	AJ262031
C	22	16.8	84.0	414	9	AJ262158
C	23	16.8	84.0	417	9	AJ262205
C	24	16.8	84.0	419	9	AJ268689
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C	37	16.8	84.0	511	17	AQ85844
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ALIGNMENTS

RESULT 1
AA362428/c

LOCUS AA362428

DEFINITION EST72059 Monocytes, stimulated 11 Homo sapiens

ACCESSION AA362428

VERSION AA362428.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 268)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A.,

Gneltun,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,

Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,

Kunsch,C., Hwangjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,

Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon

,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

268 bp mRNA linear EST 21-APR-1997
tumor necrosis factor receptor 2, mRNA sequence.

AA362428.1 GI:2014757

AA362428.1

AA362428.1

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TITLE
JOURNAL
MEDLINE
COMMENT

Venter, J.C.
 Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl.), 3-174 (1995)
 96026280
 Other ESTs: THCL166535
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source

BASE COUNT 65 a 96 c 62 g 43 t 2 others
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Query Match 100.0%; Score 20; DB 9; Length 268;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ACACCACGCTCGATGTTTCA 20
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Db 31 ACACCACGCTCGATGTTTCA 12

RESULT 2
BF764027
LOCUS BF764027 419 bp mRNA linear EST 12-JAN-2001
DEFINITION IL2-CS0048-301000-198-F06 CS0048 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF764027
VERSION BF764027.1 GI:12111927
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 419)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-CS0048-301000-198-F06&t3=2000-10-30&t4=1>)

FEATURES
 source

Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 418.
 Locat on/Qualifiers
 1. .419
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CS0048"
 /dev_stage="Adult"

/note="Organ: colon_est; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

BASE COUNT 75 a 122 c 136 g 86 t
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 419;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ACACCACGCTCGATGTTTCA 20
 |||||||||||||||||||
Db 227 ACACCACGCTCGATGTTTCA 246

RESULT 3
AW856055/c
LOCUS AW856055 485 bp mRNA linear EST 19-MAY-2000
DEFINITION RCI-CT0286-060200-015-d07 CT0286 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW856055
VERSION AW856055.1 GI:7951748
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 485)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 , M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC1-CT0286-060200-015-d07&t3=2000-02-06&t4=1>)

Seq primer: puc 18 forward
High quality sequence start: 6
High quality sequence stop: 485.
Location/Qualifiers
 1. .485

FEATURES
 source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0286"
 /dev_stage="Adult"
 /note="Organ: colon;
 SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 116 a 153 c 122 g 94 t
ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
|||||
Db 41 ACACCACGCTCTGATGTTTCA 22

RESULT 4

BF204631/c

LOCUS 601867053F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109677 5',
EST. 06-NOV-2000
mRNA sequence.

ACCESSION BF204631

VERSION BF204631.1 GI:11098217

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 652)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM994 row: j column: 14

High quality sequence stop: 650.

FEATURES Location/Qualifiers

source

1. .652

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:4109677"

/clone_lib="NIH_MGC_17"

/tissue_type="rhabdomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;

Site_2: XhoI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 121 a 215 c 215 g 101 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 652;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20

|||||

Db 471 ACACCACGCTCTGATGTTTCA 452

RESULT 5

BG828205/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG828205 741 bp mRNA linear EST 22-MAY-2001
60275359F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4905910 5',
mRNA sequence.

ACCESSION BG828205

VERSION BG828205.1 GI:14175780

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 741)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1808 row: b column: 23

High quality sequence stop: 741.

FEATURES Location/Qualifiers

1. .741

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="IMAGE:4905910"

/clone_lib="NIH_MGC_17"

/tissue_type="rhabdomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;

Site_2: XhoI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 141 a 261 c 228 g 111 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 741;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20

|||||

Db 471 ACACCACGCTCTGATGTTTCA 452

RESULT 6

BE299738/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BE299738 777 bp mRNA linear EST 20-JUL-2000
60094439F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960374 5',
mRNA sequence.

ACCESSION BE299738

VERSION BE299738.1 GI:9183486

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 777)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM53 row: j column: 23
 High quality sequence stop: 776.
 Location/Qualifiers

FEATURES

source

1..777
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2960374"
 /clone_lib="NIH_MGC_17"
 /tissue_type="rhabdomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
 Site_2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 145 a 260 c 232 g 140 t

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 777;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACACCACGCTCTGATGTTTCA 20
 ||||||||||||||||
 Db 460 ACACCACGCTCTGATGTTTCA 441

RESULT 7

BI115162/c
 LOCUS 781 bp mRNA linear EST 26-JUN-2001
 DEFINITION 602863085F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:5022068 5',
 mRNA sequence.
 ACCESSION BI115162
 VERSION BI115162.1 GI:14566063
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: ATCC

REFERENCE

AUTHORS cDNA Library Preparation: Ling Hong/Rubin Laboratory
 TITLE cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 JOURNAL DNA Sequencing by: Incyte Genomics, Inc.
 COMMENT Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1841 row: j column: 21
 High quality sequence stop: 744.
 Location/Qualifiers

FEATURES

source

1..781
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5022068"
 /clone_lib="NIH_MGC_17"
 /tissue_type="rhabdomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
 Site_2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 156 a 253 c 245 g 127 t

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 781;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACACCACGCTCTGATGTTTCA 20
 ||||||||||||||||
 Db 470 ACACCACGCTCTGATGTTTCA 451

RESULT 8

BI822108/c
 LOCUS 807 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603039994F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181070 5',
 mRNA sequence.
 ACCESSION BI822108
 VERSION BI822108.1 GI:15933658
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM11451 row: k column: 23
 High quality sequence stop: 801.
 Location/Qualifiers

FEATURES

source
 1..807
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5181070"
 /clone_lib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research genetics tracking code
 021. Note: this is a NIH_MGC Library."
 BASE COUNT 157 a 283 c 240 g 127 t

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 807;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACACCACGCTCTGATGTTTCA 20
 ||||||||||||||||
 Db 543 ACACCACGCTCTGATGTTTCA 524

RESULT 9


```

BF310740/c
LOCUS      BF310740      982 bp      mRNA      linear      EST 21-NOV-2000
DEFINITION 601895733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124840 5',
            mRNA sequence.
ACCESSION  BF310740
VERSION     BF310740.1 GI:11258352
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 982)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/,
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: L1CM1012 row: b column: 09
            High quality sequence stop: 691.
FEATURES   Location/Qualifiers
            source          1..982
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:4124840"
                        /clone_lib="NIH_MGC_19"
                        /tissue_type="neuroblastoma"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: brain; Vector: pOTB7; site_1: XhoI; site_2:
                        EcoRI; cDNA made by oligo-dT priming. Directionally
                        cloned into EcoRI/XhoI sites using the following 5'
                        adaptor: GGCACGAG(G). Library constructed by Ling Hong
                        in the laboratory of Gerald M. Rubin (University of
                        California, Berkeley) using ZAP-cDNA synthesis kit
                        (Stratagene) and Superscript II RT (Life Technologies).
                        Note: this is a NIH_MGC Library."
BASE COUNT 222 a 246 c 316 g 198 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 982;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCGATGTTTCA 20
    |||||
DB 495 ACACCACGCTCGATGTTTCA 476

RESULT 10
BG109353/c
LOCUS      BG109353      1177 bp      mRNA      linear      EST 30-JAN-2001
DEFINITION 602280404F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4368025 5',
            mRNA sequence.
ACCESSION  BG109353
VERSION     BG109353.1 GI:12602859
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1177)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/,
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
JOURNAL     Contact: Robert Strausberg, Ph.D.
COMMENT     Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.

```

```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10021 row: g column: 02
High quality sequence stop: 705.
FEATURES   Location/Qualifiers
            source          1..1177
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:4368025"
                        /clone_lib="NIH_MGC_86"
                        /tissue_type="osteosarcoma, cell line"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                        Average insert size 1.533 kb. Library enriched for
                        full-length clones and constructed by Life Technologies.
                        Note: this is a NIH_MGC Library."
BASE COUNT 293 a 365 c 353 g 166 t
ORIGIN
Query Match      100.0%; Score 20; DB 12; Length 1177;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCGATGTTTCA 20
    |||||
DB 442 ACACCACGCTCGATGTTTCA 423

RESULT 11
BC011844/c
LOCUS      BC011844      2291 bp      mRNA      linear      HTC 02-AUG-2001
DEFINITION Homo sapiens, Similar to tumor necrosis factor receptor
            superfamily, member 1B, clone IMAGE:4111730, mRNA.
ACCESSION  BC011844
VERSION     BC011844.1 GI:15080140
KEYWORDS    HTC.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2291)
AUTHORS    Strausberg, R.
TITLE      Direct Submission
JOURNAL     Submitted (30-JUL-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland.
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
            Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
            Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
            Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
            McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
            Tngson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
            Zhang, L.-H. and Green, E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 28 Row: 1 Column: 15

```

This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
 This clone has the following problem: incomplete processing.

```

FEATURES             source
  source
    Location/Qualifiers
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:411730"
      /tissue_type="Muscle, rhabdomyosarcoma"
      /clone_lib="NIH_MGC_17"
      /lab_host="DH10B-R"
      /note="Vector: pOTB7"
BASE COUNT          461 a 708 c 713 g 409 t
ORIGIN
Query Match          100.0%; Score 20; DB 11; Length 2291;
Best Local Similarity 100.0%; Pred. NO. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCAGCTCTGATGTTTCA 20
|||||
Db 479 ACACCAGCTCTGATGTTTCA 460

RESULT 12
AJ272769/c           680 bp mRNA linear EST 29-DEC-1999
LOCUS
DEFINITION
  cDNA clone Ma#92, mRNA sequence.
ACCESSION
  AJ272769
VERSION
  AJ272769.1 GI:6432142
KEYWORDS
  EST.
SOURCE
  Metarhizium anisopliae.
  ORGANISM
    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
    Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae;
    Metarhizium.
  1 (bases 1 to 680)
  Screen, S.E., Mathur, P. and St. Leger, R.J.
  EST analysis of the insect pathogenic fungus Metarhizium anisopliae
  Unpublished (1999)
  Contact: Screen SE
  Entomology
  University of Maryland
  4112 Plant Sciences Building, College Park, MD 20742, USA.
FEATURES             source
  source
    Location/Qualifiers
      /organism="Metarhizium anisopliae"
      /strain="ARSEF 2575"
      /db_xref="taxon:5530"
      /clone="Ma#92"
      /clone_lib="Metarhizium anisopliae ARSEF 2575"
      /note="Vector: Unizap; Metarhizium anisopliae was grown on
      insect cuticle for 24 hours. A cDNA library was
      constructed in the unidirectional Lambda vector, Unizap"
BASE COUNT          157 a 177 c 183 g 159 t
ORIGIN
Query Match          90.0%; Score 18; DB 9; Length 680;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCAGCTCTGATGTTTC 19
|||||
Db 160 CACCAGCTCTGATGTTTC 143

RESULT 13
BQ924155/c           1097 bp mRNA linear EST 20-AUG-2002
LOCUS
DEFINITION
  AGENCOURT_8877927 Lupski_sciatic_nerve Homo sapiens cDNA clone
  IMAGE:6198614 5', mRNA sequence.

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ACCESSION            BQ924155
VERSION               BQ924155.1 GI:22339186
KEYWORDS
SOURCE
  Homo sapiens
  human.
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  1 (bases 1 to 1097)
  NIH-MGC http://mgi.nci.nih.gov/
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Dr. James R. Lupski
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: LLAM13610 row: i column: 15
  High quality sequence stop: 492.
  Location/Qualifiers
    1..1097
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:6198614"
    /clone_lib="Lupski_sciatic_nerve"
    /sex="male"
    /tissue_type="sciatic nerve"
    /dev_stage="adult, 70 yr"
    /lab_host="DH10B"
    /note="Vector: PCMV-SPORT6 (Life Technologies); Site_1:
    NotI; Site_2: SalI; cDNA made by oligo-dT priming.
    Directionally cloned using the following adaptors:
    5'-TCGACCCACGCGTCG-3' and
    5'-GACTAGTTCTAGATCGGAGCGCGCCT(15)-3'. Size selected >
    1 kb for average insert length 1.87 kb. This is a primary
    library, non-amplified. Library constructed by Life
    Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
    College of Medicine) and is available through Life
    Technologies."
BASE COUNT           183 a 351 c 427 g 136 t
ORIGIN
Query Match          87.0%; Score 17.4; DB 14; Length 1097;
Best Local Similarity 94.7%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CACCAGCTCTGATGTTTCA 20
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Db 562 CACCAGCTCTGATGTTTCA 544

RESULT 14
AQ816262/c           301 bp DNA linear GSS 26-AUG-1999
LOCUS
DEFINITION
  HS_5498_A2_E01_SP6E RPCI-11 Human Male BAC Library Homo sapiens
  genomic clone Plate-1074 Col-2 Row=I, DNA sequence.
ACCESSION            AQ816262
VERSION               AQ816262.1 GI:5778655
KEYWORDS
  GSS.
SOURCE
  human.
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  1 (bases 1 to 301)
  Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
  Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
  Hood, L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

```

MEDLINE
COMMENT

99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: <http://www.hsc.washington.edu>
Plate: 1074 row: 1 column: 2
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 301.

FEATURES
source

Location/Qualifiers
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/clone="plate=1074 Col=2 Row=1"
/clone.lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 102 a 62 c 73 g 64 t
ORIGIN

Query Match 85.0%; Score 17; DB 17; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCACGCTCTGATGTTT 18
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Db 121 CACCACGCTCTGATGTTT 105

RESULT 15

BF203997/c

LOCUS 601869116F1 NIH_MGC_17 780 bp mRNA linear EST 06-NOV-2000
DEFINITION mRNA sequence.

ACCESSION BF203997

VERSION BF203997.1 GI:11097583

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 780)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM999 row: p column: 03

High quality sequence stop: 679.

FEATURES

source

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:4111730"

/clone.lib="NIH_MGC_17"
/tissue_type="rhadomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected by
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 161 a 214 c 254 g 150 t
ORIGIN

Query Match 85.0%; Score 17; DB 12; Length 780;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTT 17
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Db 506 ACACCACGCTCTGATGTTT 490

Search completed: December 6, 2002, 04:54:20
Job time : 50.2783 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 ; Search time 1.03896 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-3

Perfect score: 20

Sequence: 1 acaccagctctgatgtttca 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_NA.*
- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
 - 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
 - 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
 - 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
 - 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	36	6	Patent No. 5395760
C 2	20	100.0	691	1	US-08-266-080B-12
C 3	20	100.0	691	5	PCT-US95-05423-12
C 4	20	100.0	705	4	US-09-326-394-3
C 5	20	100.0	705	4	US-09-580-235-1
C 6	20	100.0	705	4	US-09-580-235-3
C 7	20	100.0	705	4	US-09-580-235-5
C 8	20	100.0	705	4	US-09-580-235-7
C 9	20	100.0	705	4	US-09-580-181-1
C 10	20	100.0	705	4	US-09-580-181-3
C 11	20	100.0	705	4	US-09-580-181-5
C 12	20	100.0	705	4	US-09-580-181-7
C 13	20	100.0	705	4	US-09-102-530-1
C 14	20	100.0	705	4	US-09-102-530-3
C 15	20	100.0	705	4	US-09-102-530-5
C 16	20	100.0	705	4	US-09-102-530-7
C 17	20	100.0	1557	1	US-08-385-229-3
C 18	20	100.0	1641	1	US-08-385-229-1
C 19	20	100.0	1641	2	US-08-650-000-1
C 20	20	100.0	1641	6	5395760-1
C 21	20	100.0	2224	4	US-08-477-347-2
C 22	20	100.0	2224	4	US-08-476-862-1
C 23	20	100.0	3683	4	US-09-844-634-3
C 24	19	95.0	34	1	US-08-050-319B-23
C 25	19	95.0	34	2	US-08-465-982-23
C 26	17	85.0	20	4	US-09-844-634-35
C 27	15.8	79.0	1712	2	US-08-632-598-1

C 28	15.8	79.0	1712	4	US-09-231-240-1	Sequence 1, Appli
C 29	14.8	74.0	2074	3	US-08-301-162-17	Sequence 17, Appl
C 30	14.8	74.0	2074	4	US-09-461-240-17	Sequence 17, Appl
C 31	14.8	74.0	2074	4	US-09-968-927-17	Sequence 17, Appl
C 32	14.4	72.0	1958	4	US-09-453-702B-113	Sequence 113, App
C 33	14.4	72.0	3321	1	US-08-486-270-1	Sequence 1, Appli
C 34	14.4	72.0	3321	3	US-08-367-264-1	Sequence 1, Appli
C 35	14.4	72.0	3321	4	US-09-153-757-1	Sequence 1, Appli
C 36	14.4	72.0	3330	1	US-08-072-574-1	Sequence 1, Appli
C 37	14.4	72.0	3582	4	US-08-538-526-2	Sequence 2, Appli
C 38	14.2	71.0	860	4	US-08-998-416-546	Sequence 546, App
C 39	14.2	71.0	1099	1	US-08-181-271A-25	Sequence 25, Appl
C 40	14.2	71.0	1099	1	US-08-449-315-25	Sequence 25, Appl
C 41	14.2	71.0	1099	1	US-08-444-803-25	Sequence 25, Appl
C 42	14.2	71.0	1099	1	US-08-449-043-25	Sequence 25, Appl
C 43	14.2	71.0	1099	1	US-08-456-265A-25	Sequence 25, Appl
C 44	14.2	71.0	1099	1	US-08-455-416-25	Sequence 25, Appl
C 45	14.2	71.0	1099	1	US-08-455-244-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
5395760-14/c
; Patent No. 5395760
; APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
; M. PATRICIA
; TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-A AND
; B-RECEPTORS
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/523,635
; FILING DATE: 10-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 421,417
; FILING DATE: 13-OCT-1989
; APPLICATION NUMBER: 405,370
; FILING DATE: 11-SEP-1989
; APPLICATION NUMBER: 403,241
; FILING DATE: 05-SEP-1989
; SEQ ID NO:14:
; LENGTH: 36
5395760-14

Query Match 100.0%; Score 20; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCAGCTCTGATGTTTCA 20
Db 21 ACACCAGCTCTGATGTTTCA 2

RESULT 2
US-08-266-080B-12/c
; Sequence 12, Application US/08266080B
; Patent No. 5606031
; GENERAL INFORMATION:
; APPLICANT: Jack Lille
; APPLICANT: Tadabiko Kohno
; APPLICANT: Duane Bonam
; APPLICANT: Mary S. Rosendahl
; TITLE OF INVENTION: Production of Biologically Active
; RECOMBINANT Neurotrophic Protein
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,080B
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
TELEPHONE: (303) 793-3333
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: SYNE200C5
TELEPHONE: (303) 793-3333
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-266-080B-12

Query Match 100.0%; Score 20; DB 1; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGTGATGTTTCA 20
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Db 553 ACACCACGCTGTGATGTTTCA 534

RESULT 3
PCT-US95-05423-12/c
Sequence 12, Application PC/TUS9505423
GENERAL INFORMATION:
APPLICANT: Jack Lile
APPLICANT: Tadahiko Kohno
APPLICANT: Duane Bonam
APPLICANT: Mary S. Rosendahl
TITLE OF INVENTION: Production of Biologically Active
TITLE OF INVENTION: Recombinant Neurotrophic Protein
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05423
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/266,090
FILING DATE: 27-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,122
FILING DATE: 09-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,912
FILING DATE: 06-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/680,681
FILING DATE: 04-APRIL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/594,126
FILING DATE: 09-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/547,750
FILING DATE: 02-JULY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/505,441
FILING DATE: 06-APRIL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: SYNE200/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05423-12

Query Match 100.0%; Score 20; DB 5; Length 691;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGTGATGTTTCA 20
|||||
Db 553 ACACCACGCTGTGATGTTTCA 534

RESULT 4
US-09-326-394-3/c
Sequence 3, Application US/09326394
Patent No. 6306820
GENERAL INFORMATION:
APPLICANT: Bendele, Allison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Edwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: CA
COUNTRY: US
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,394

;; FILING DATE: 08-DEC-1997
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/032,587
;; FILING DATE: 06-DEC-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/036,355
;; FILING DATE: 23-JAN-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/039,315
;; FILING DATE: 07-FEB-1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/052,023
;; FILING DATE: 09-JUL-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zindrick, Thomas K.
;; REGISTRATION NUMBER: 32,185
;; REFERENCE/DOCKET NUMBER: A-430D
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 705 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..705
US-09-326-394-3

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGATGTTTCA 20
|||||
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 5
US-09-580-235-1/c
; Sequence 1, Application US/09580235
; Patent No. 6433158
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/102,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-326-394-3

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 705 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..705
US-09-580-235-1

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGATGTTTCA 20
|||||
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 6
US-09-580-235-3/c
; Sequence 3, Application US/09580235
; Patent No. 6433158
; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,235
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/102,530
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-235-3

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGATGTTTCA 20
|||||
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 7

US-09-580-235-5/c

; Sequence 5, Application US/09580235

; Patent No. 6433158

; GENERAL INFORMATION:

; APPLICANT: Pettit, Dean

; TITLE OF INVENTION: Site Specific Protein Modification

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Janis C Henry

; STREET: 51 University

; CITY: Seattle

; STATE: WA

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/580,235

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/102,530

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Henry, Janis C

; REGISTRATION NUMBER: 34,347

; REFERENCE/DOCKET NUMBER: 2637

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)470-4189

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 705 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..705

; US-09-580-235-5

Query Match

; Sequence 7, Application US/09580235

; Patent No. 6433158

; GENERAL INFORMATION:

; APPLICANT: Pettit, Dean

; TITLE OF INVENTION: Site Specific Protein Modification

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

RESULT 8

US-09-580-235-7/c

; Sequence 7, Application US/09580235

; Patent No. 6433158

; GENERAL INFORMATION:

; APPLICANT: Pettit, Dean

; TITLE OF INVENTION: Site Specific Protein Modification

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; APPLICATION NUMBER: US 09/102,530
; FILING DATE: 22-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-181-1

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
|||||
DB 415 ACACCACGCTGATGTTTCA 396

RESULT 10

US-09-580-181-3/c
; Sequence 3, Application US/09580181
; Patent No. 6441136

; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580.181
; FILING DATE: 26-MAY-2000

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/102,530
; FILING DATE: 22-JUN-1998

; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-09-580-181-3

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
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DB 415 ACACCACGCTGATGTTTCA 396

RESULT 11

US-09-580-181-5/c
; Sequence 5, Application US/09580181
; Patent No. 6441136

; GENERAL INFORMATION:
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Site Specific Protein Modification
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C Henry
; STREET: 51 University
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580.181
; FILING DATE: 26-MAY-2000

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/102,530
; FILING DATE: 22-JUN-1998

; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2637

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: N-terminal

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705

US-09-580-181-5

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
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DB 415 ACACCACGCTGATGTTTCA 396

RESULT 12

US-09-580-181-7/c
: Sequence 7, Application US/09580181
: Patent No. 6441136
: GENERAL INFORMATION:
: APPLICANT: Pettit, Dean
: TITLE OF INVENTION: Site Specific Protein Modification
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C Henry
: STREET: 51 University
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/580,181
: FILING DATE: 26-MAY-2000
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/102,530
: FILING DATE: 22-JUN-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2637
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..705
US-09-580-181-7

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGTGATGTTTCA 20
|||||
Db 415 ACACCACGCTGTGATGTTTCA 396

RESULT 13

US-09-102-530-1/c
: Sequence 1, Application US/09102530
: Patent No. 6451986
: GENERAL INFORMATION:
: APPLICANT: Pettit, Dean
: TITLE OF INVENTION: Site Specific Protein Modification
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C Henry
: STREET: 51 University
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/102,530
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2637
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..705
US-09-102-530-1

Query Match 100.0%; Score 20; DB 4; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACACCACGCTGTGATGTTTCA 20
|||||
Db 415 ACACCACGCTGTGATGTTTCA 396

RESULT 14

US-09-102-530-3/c
: Sequence 3, Application US/09102530
: Patent No. 6451986
: GENERAL INFORMATION:
: APPLICANT: Pettit, Dean
: TITLE OF INVENTION: Site Specific Protein Modification
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Janis C Henry
: STREET: 51 University
: CITY: Seattle
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/102,530
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Henry, Janis C
: REGISTRATION NUMBER: 34,347
: REFERENCE/DOCKET NUMBER: 2637
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)470-4189
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 705 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single

QY 1 ACACCACGCTCTGATGTTTCA 20
|||||
Db 415 ACACCACGCTCTGATGTTTCA 396

GenCore version 5.1.3
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OM nucleic - nucleic search, using sv model

Run on: December 5, 2002, 20:03:23 ; Search time 0.972171 Seconds
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Title: us-09-856-937A-3

Perfect score: 20

Sequence: 1 aacaccagctctgatgttca 20

Scoring table: IDENTITY_NUC

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Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	20	100.0	1641	10	US-09-758-124-1
C 3	20	100.0	2224	10	US-09-800-909-1
C 4	20	100.0	2224	10	US-09-800-908-2
C 5	20	100.0	3683	10	US-09-954-456-1187
C 6	15.8	79.0	306	10	US-09-974-300-3873
C 7	15.8	79.0	474	10	US-09-864-761-591
C 8	15.2	76.0	601	10	US-09-828-644-28
C 9	15.2	76.0	1659	10	US-09-740-288A-29
C 10	15.2	76.0	5617	10	US-09-917-800A-496
C 11	15.2	76.0	5921	12	US-10-040-919-1
C 12	15.2	76.0	6183	10	US-09-866-562-50
C 13	15.2	76.0	16428	10	US-09-764-847-1613
C 14	15.2	76.0	31834	10	US-09-764-847-1612
C 15	15.2	76.0	32035	10	US-09-764-847-1611
C 16	15.2	76.0	143306	10	US-09-729-920-3
C 17	14.8	74.0	237	9	US-09-783-590-8279
C 18	14.8	74.0	321	9	US-10-046-935-1825
C 19	14.8	74.0	321	9	US-09-878-178-1825

20	14.8	74.0	361	10	US-09-738-973-365	Sequence 365, App
21	14.8	74.0	456	10	US-09-960-352-1047	Sequence 1047, App
C 22	14.8	74.0	7215	10	US-09-070-927A-102	Sequence 102, App
C 23	14.8	74.0	7497	10	US-09-960-253-175	Sequence 175, App
C 24	14.8	74.0	7792	12	US-10-044-090-359	Sequence 359, App
C 25	14.8	74.0	48667	10	US-09-822-268A-3	Sequence 3, Appl
C 26	14.4	72.0	109	10	US-09-864-761-18345	Sequence 18345, A
C 27	14.4	72.0	387	10	US-09-864-761-1587	Sequence 1587, App
C 28	14.4	72.0	437	10	US-09-960-352-10610	Sequence 10610, A
C 29	14.2	71.0	372	10	US-09-770-791-329	Sequence 329, App
C 30	14.2	71.0	448	10	US-09-867-701-3249	Sequence 3249, App
C 31	14.2	71.0	467	10	US-09-867-701-2779	Sequence 2779, App
C 32	14.2	71.0	497	9	US-10-046-935-796	Sequence 796, App
C 33	14.2	71.0	497	9	US-09-878-178-796	Sequence 796, App
C 34	14.2	71.0	529	10	US-09-867-701-5479	Sequence 5479, App
C 35	14.2	71.0	537	10	US-09-070-927A-810	Sequence 810, App
C 36	14.2	71.0	553	9	US-10-046-935-1370	Sequence 1370, App
C 37	14.2	71.0	553	9	US-09-878-178-1370	Sequence 1370, App
C 38	14.2	71.0	595	10	US-09-777-564-619	Sequence 619, App
C 39	14.2	71.0	595	10	US-09-777-564-1452	Sequence 1452, App
C 40	14.2	71.0	723	10	US-09-878-574-4760	Sequence 4760, App
C 41	14.2	71.0	1224	10	US-09-730-525-21	Sequence 21, Appl
C 42	14.2	71.0	1224	10	US-09-730-917-21	Sequence 21, Appl
C 43	14.2	71.0	1455	10	US-09-815-242-6712	Sequence 6712, App
C 44	14.2	71.0	1658	9	US-10-002-344A-31	Sequence 31, Appl
C 45	14.2	71.0	1876	10	US-09-729-402-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-907-263-3/c

; Sequence 3, Application US/09907263

; Patent No. US20020119924A1

; GENERAL INFORMATION:

; APPLICANT: Bendele, Allison M.

; Sennello, Regina M.

; Edwards, Carl K.

; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING

; PROTEIN FOR TREATING TNF-MEDIATED DISEASES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 DeHavilland Drive

; CITY: Thousand Oaks

; STATE: CA

; COUNTRY: US

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION NUMBER: US/09/907,263

; FILING DATE: 17-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/326,394

; FILING DATE: 1999-06-04

; APPLICATION NUMBER: US 60/036,355

; FILING DATE: 23-JAN-1997

; APPLICATION NUMBER: US 60/039,315

; FILING DATE: 07-FEB-1997

; APPLICATION NUMBER: US 60/052,023

; FILING DATE: 09-JUL-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Zindrick, Thomas K.

; REGISTRATION NUMBER: 32,185

; REFERENCE/DOCKET NUMBER: A-430D

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

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; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-907-263-3

Query Match      100.0%; Score 20; DB 10; Length 705;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
Db 415 ACACCACGCTGATGTTTCA 396

RESULT 2
US-09-758-124-1/c
; Sequence 1, Application US/09758124
; Patent No. US20020006391A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, Craig A.
; APPLICANT: GOODWIN, Raymond G.
; APPLICANT: BECKMANN, M. Patricia
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
; FILE REFERENCE: A7895
; CURRENT APPLICATION NUMBER: US/09/758,124
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 08/953,268
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 08/555,629
; PRIOR FILING DATE: 1995-11-09
; PRIOR APPLICATION NUMBER: 08/468,453
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/038,765
; PRIOR FILING DATE: 1993-03-13
; PRIOR APPLICATION NUMBER: 07/523,635
; PRIOR FILING DATE: 1990-05-10
; PRIOR APPLICATION NUMBER: 07/421,417
; PRIOR FILING DATE: 1989-10-13
; PRIOR APPLICATION NUMBER: 07/405,370
; PRIOR FILING DATE: 1989-09-11
; PRIOR APPLICATION NUMBER: 07/403,241
; PRIOR FILING DATE: 1989-09-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 1641
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1473)
; NAME/KEY: mat_peptide
; LOCATION: (154)..(1470)
; NAME/KEY: sig_peptide
; LOCATION: (88)..(153)
US-09-758-124-1

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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
Db 568 ACACCACGCTGATGTTTCA 549

RESULT 3
US-09-800-909-1/c
; Sequence 1, Application US/09800909
; Patent No. US20010019833A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,909
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,862
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=12A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
US-09-800-909-1

Query Match      100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACCACGCTGATGTTTCA 20
Db 570 ACACCACGCTGATGTTTCA 551

RESULT 4
US-09-800-908-2/c
; Sequence 2, Application US/09800908
; Patent No. US2002011462A1
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
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;
; BIGDA, Jacek
; BELETSKY, Igor
; METT, Igor
; TITLE OF INVENTION: TNF LIGANDS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/800,908
; FILING DATE: 08-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,347
; FILING DATE: <Unknown>
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 90..1472
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-800-908-2

Query Match 100.0%; Score 20; DB 10; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACACGCTCTGATGTTTCA 20
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Db 570 ACACACGCTCTGATGTTTCA 551

RESULT 5
US-09-954-456-1187/c
; Sequence 1187, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25

;
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1187
; LENGTH: 3683
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-954-456-1187

Query Match 100.0%; Score 20; DB 10; Length 3683;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACACACGCTCTGATGTTTCA 20
||| ||||| ||||| ||||| |||||
Db 570 ACACACGCTCTGATGTTTCA 551

RESULT 6
US-09-974-300-3873/c
; Sequence 3873, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3873
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; US-09-974-300-3873

Query Match 79.0%; Score 15.8; DB 10; Length 306;
Best Local Similarity 89.5%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACGCTCTGATGTTTCA 20
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Db 137 CACACGCTCTGATGTTTCA 119

RESULT 7
US-09-864-761-591
; Sequence 591, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

```

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 591
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007656.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; US-09-864-761-591

Query Match 79.0%; Score 15.8; DB 10; Length 474;
Best Local Similarity 89.5%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ACACACGCTCTGATGTTTC 19
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Db 243 ACACCATTTCTGATGTTTC 261

RESULT 8
US-09-828-644-28
; Sequence 28, Application US/09828644

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 591
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007656.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; US-09-864-761-591

Query Match 79.0%; Score 15.8; DB 10; Length 474;
Best Local Similarity 89.5%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 ACACACGCTCTGATGTTTC 19
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Db 243 ACACCATTTCTGATGTTTC 261

RESULT 8
US-09-828-644-28
; Sequence 28, Application US/09828644

; Patent No. US20020015998A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: NO. US20020015998A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00196US1
; CURRENT APPLICATION NUMBER: US/09/828,644
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,150
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,099
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,151
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,148
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,093
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,098
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/230,149
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-828-644-28

Query Match 76.0%; Score 15.2; DB 10; Length 601;
Best Local Similarity 85.0%; Pred. No. 46;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ACACCACGCTCTGATGTTTCA 20
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Db 573 ACACCAAGGCTGATGTTTCA 592

RESULT 9
US-09-740-288A-29
; Sequence 29, Application US/09740288A
; Patent No. US20010039042A1
; GENERAL INFORMATION:
; APPLICANT: Kinney, Stephen
; APPLICANT: Allen, Stephen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Orozco, Emil
; TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
; FILE REFERENCE: BB1429 US NA
; CURRENT APPLICATION NUMBER: US/09/740,288A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 60/172929
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
; LENGTH: 1659
; TYPE: DNA
; ORGANISM: Glycine max
; US-09-740-288A-29

Query Match 76.0%; Score 15.2; DB 10; Length 1659;
Best Local Similarity 85.0%; Pred. No. 55;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ACACCACGCTCTGATGTTTCA 20
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Db 1069 ACAACAGGCTCTTATGTTTCA 1088

RESULT 10
US-09-917-800A-496/c
; Sequence 496, Application US/09917800A
```

; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 496
; LENGTH: 5617
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AF052695
US-09-917-800A-496

Query Match 76.0%; Score 15.2; DB 10; Length 5617;
Best Local Similarity 85.0%; Pred. No. 68;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
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DB 1689 ACACCAGTCTCATGCTCTCA 1670

RESULT 11
US-10-040-919-1
; Sequence 1, Application US/10040919
; Patent No. US20020150563A1
; GENERAL INFORMATION:
; APPLICANT: Bowman, Michael
; APPLICANT: Lohmar, Patricia D.
; APPLICANT: Wood, Nancy L.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: GPI-122, A No. US20020150563A1e1 Glycophosphatidylinositol-Anchored Protein
; FILE REFERENCE: GI 5312A
; CURRENT APPLICATION NUMBER: US/10/040,919
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/277,837
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 5921
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-919-1

Query Match 76.0%; Score 15.2; DB 12; Length 5921;
Best Local Similarity 85.0%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
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DB 3579 AACCCACGTCGGATGTTTCA 3598

RESULT 12
US-09-866-562-50/c
; Sequence 50, Application US/09866562
; Patent No. US20020009758A1
; GENERAL INFORMATION:
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Klee, Jennifer
; APPLICANT: Switzer, Anne
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.502
; CURRENT APPLICATION NUMBER: US/09/866,562
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 50
; LENGTH: 6183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-562-50

Query Match 76.0%; Score 15.2; DB 10; Length 6183;
Best Local Similarity 85.0%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
||||| ||||| ||||| ||||| |||||

DB 4703 ACACCAAGTCTTATTTTCA 4684

RESULT 13
US-09-764-847-1613/c
; Sequence 1613, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1613
; LENGTH: 16428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1613

Query Match 76.0%; Score 15.2; DB 10; Length 16428;
Best Local Similarity 85.0%; Pred. No. 82;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACACCACGCTCTGATGTTTCA 20
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DB 8425 ACACCTCGTCTCATATTTCA 8406

RESULT 14
US-09-764-847-1612/c
; Sequence 1612, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1612
; LENGTH: 31834
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1612

Query Match 76.0%; Score 15.2; DB 10; Length 31834;
Best Local Similarity 85.0%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACACCACGCTCTGATGTTTCA 20
||||| ||||| || |||||
Db 24037 ACACCTCGTCTCATATTTC 24018

RESULT 15
US-09-764-847-1611/c
; Sequence 1611, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1611
; LENGTH: 32035
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1611

Query Match 76.0%; Score 15.2; DB 10; Length 32035;
Best Local Similarity 85.0%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACACCACGCTCTGATGTTTCA 20
||||| ||||| || |||||
Db 24031 ACACCTCGTCTCATATTTC 24012

Search completed: December 6, 2002, 00:18:00
Job time : 21.9722 secs

GenCore version 5.1.3
Copyright (c) 1993 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:30:25 : Search time 41.4471 seconds
(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937A-4

Perfect score: 20
Sequence: 1 aggactctgagcgtctttct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GeneBlast:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_pi.*
- 8: gb_pr.*
- 9: gb_ro.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_on.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	480	9	AB030952	AB030952 Homo sapi
2	20	100.0	870	11	G15915	G15915 human STS C
3	20	100.0	1641	6	I36196	I36196 Sequence 1
4	20	100.0	2224	6	AR152033	AR152033 Sequence 1
5	20	100.0	2253	6	A78517	A78517 Sequence 1
6	20	100.0	2339	6	A26415	A26415 cDNA fragme
7	20	100.0	2394	9	HUMTNR11	M55994 Human tumor
8	20	100.0	2613	9	HSTNFR2S10	U52165 Human tumor
9	20	100.0	3380	11	G26865	G26865 human STS S
10	20	100.0	3492	9	S63368	S63368 Homo sapien
11	20	100.0	3683	6	AX333705	AX333705 Sequence
12	20	100.0	3683	6	AX348016	AX348016 Sequence
13	20	100.0	3683	6	AX348018	AX348018 Sequence
14	20	100.0	3683	6	AX348020	AX348020 Sequence
15	20	100.0	3683	9	HUMNFR	M32315 Human tumor
16	20	100.0	115602	9	HS1118D24	AL031276 Human DNA
17	20	100.0	122105	2	AL355998	AL355998 Homo sapi
18	20	100.0	187877	2	AC023251	AC023251 Homo sapi
19	19	95.0	25	6	AX348010	AX348010 Sequence
20	19	95.0	166555	2	AC009197	AC009197 Rattus no
21	19	95.0	188314	9	AC009494	AC009494 Homo sapi
22	19	95.0	230334	10	AC112521	AC112521 Mus muscu
23	18.4	92.0	104630	9	AC007397	AC007397 Homo sapi
24	18.4	92.0	108778	9	AC005194	AC005194 Homo sapi
25	18.4	92.0	110348	2	AC098539	AC098539 Rattus no
26	18.4	92.0	139398	9	AC025836	AC025836 Homo sapi
27	18.4	92.0	153360	2	AC129073	AC129073 Felis cat
28	18.4	92.0	154485	2	AC068934	AC068934 Homo sapi
29	18.4	92.0	157975	2	AC127476	AC127476 Felis cat
30	18.4	92.0	161339	9	AC007535	AC007535 Homo sapi
31	18.4	92.0	165889	10	AL606841	AL606841 Mouse DNA
32	18.4	92.0	169898	2	AC016585	AC016585 Homo sapi
33	18.4	92.0	171529	2	AC023021	AC023021 Homo sapi
34	18.4	92.0	172574	2	AC011121	AC011121 Homo sapi
35	18.4	92.0	182823	9	AC016638	AC016638 Homo sapi
36	18.4	92.0	197065	9	AC090686	AC090686 Homo sapi
37	18.4	92.0	202249	2	AC095427	AC095427 Rattus no
38	18.4	92.0	204493	2	AC111047	AC111047 Mus muscu
39	18.4	92.0	208709	2	AL592162	AL592162 Mus muscu
40	18.4	92.0	217807	2	AC079469	AC079469 Homo sapi
41	18	90.0	65792	2	AC117664	AC117664 Mus muscu
42	18	90.0	164331	9	AC016254	AC016254 Homo sapi
43	17.4	87.0	1716	5	DRAJ3200	AJ003200 Danio rer
44	17.4	87.0	1813	5	AF168008	AF168008 Danio rer
45	17.4	87.0	40036	2	AC101084	AC101084 Mus muscu

ALIGNMENTS

RESULT 1	AB030952	480 bp	DNA	linear	PRI 02-JUN-2001
LOCUS	AB030952				
DEFINITION	Homo sapiens TNFR2 gene for tumor necrosis factor receptor 2, partial cds.				
ACCESSION	AB030952				
VERSION	AB030952.1	GI:6683135			
KEYWORDS	tumor necrosis factor receptor 2; TNFR2.				
SOURCE	Homo sapiens DNA.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (sites)				
AUTHORS	Tsuchiya,N., Komata,T., Matsushita,M., Ohashi,J. and Tokunaga,K.				
TITLE	New single nucleotide polymorphisms in the coding region of human				

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

TNFR2: association with systemic lupus erythematosus
Genes Immun. 1 (8), 501-503 (2000)
21069356
2 (bases 1 to 480)
Komata,T., Tsuchiya,N. and Tokunaga,K.
Direct Submission
Submitted (09-AUG-1999) Tae Komata, University of Tokyo, Department
of Human Genetics, Graduate School of Medicine, 7-3-1 Hongo,
Bunkyo-ku, Tokyo 113-0033, Japan (E-mail:tae@m.u-tokyo.ac.jp,
Tel:81-3-5841-3693, Fax:81-3-5802-8619)

FEATURES
source
exon
gene
CDS
variation

1. .480
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
78. .>480
/number=10
78. .358
/gene="TNFR2"
<78. .358
/gene="TNFR2"
/codon_start=3
/product="tumor necrosis factor receptor 2"
/protein_id="BAA89055.1"
/db_xref="GI:6683136"
/translation="SSPGHGHTQVNVTCIVNVCSSDHSQSSQASSTMGDTSSPS
ESPKEQVPFSPKSECAFRSQLETPETLLGSTEEKPLPLGVDPAGMKPS"
381

BASE COUNT 93 a 159 c 137 g 91 t
ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 454 AGGACTCTGAGGCTCTTTCT 473

RESULT 2
GI5915
LOCUS
DEFINITION

GI5915 870 bp DNA linear STS 19-JAN-1996
human STS CHLC.UTR_02819_M32315.P65016 clone UTR_02819_M32315,
sequence tagged site.

GI5915 GI:1161804
STS; STS sequence; primer; sequence tagged site.
Homo sapiens vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker
Selected genomic DNA prepared from XY individual of French
nationality.

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H.
Cooperative Human Linkage Center
Unpublished (1995)
Synonyms: UTR_02819_M32315, CHLC.UTR_02819_M32315.T36190
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu

Primer A: CCCTGACTCTCTGTGACCTG
Primer B: GTCTTCATGGGTGACTCAGG
STS size: 206
PCR Profile: denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C

extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C

Protocol:

Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 ul

Buffer:

MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3

FEATURES
source
STS
primer_bind
primer_bind
BASE COUNT 157 a 246 c 279 g 188 t
ORIGIN

Location/Qualifiers
1. .870
/organism="Homo sapiens"
/db_xref="taxon:9606"
272. .477
272. .291
complement(458. .477)
188 t

Query Match 100.0%; Score 20; DB 11; Length 870;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 96 AGGACTCTGAGGCTCTTTCT 115

RESULT 3
I36196
LOCUS
DEFINITION

I36196 1641 bp DNA linear PAT 13-MAY-1997
Sequence 1 from patent US 5605690.

I36196
VERSION I36196.1 GI:2086709
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

1 (bases 1 to 1641)
Jacobs,C.A. and Smith,C.A.
Methods of lowering active TNF-.alpha. levels in mammals using
tumor necrosis factor receptor
Patent: US 5605690-A 1 25-FEB-1997;
Location/Qualifiers
1. .1641

BASE COUNT 328 a 544 c 502 g 267 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1641;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1569 AGGACTCTGAGGCTCTTTCT 1588

RESULT 4
AR152033
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AR152033 2224 bp DNA linear PAT 08-AUG-2001
Sequence 2 from patent US 6232446.
AR152033
AR152033.1 GI:15118083

SOURCE ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2224)
AUTHORS Wallach,D., Bigda,J., Beletsky,I., Mett,I. and Engelmann,H.
TITLE TNF ligands
JOURNAL Patent: US 6232446-A 2 15-MAY-2001;
FEATURES Location/Qualifiers
1..2224
/organism="unknown"
BASE COUNT 435 a 698 c 689 g 402 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2224;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590
RESULT 5
A78517 2253 bp DNA linear PAT 19-OCT-1999
LOCUS
DEFINITION Sequence 1 from Patent EP0585939.
ACCESSION A78517
VERSION A78517.1 GI:6090179
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2253)
AUTHORS Mett,I. and Wallach,D.
TITLE TNF LIGANDS
JOURNAL Patent: EP 0585939-A 1 09-MAR-1994;
FEATURES YEDA RES & DEV (IL)
source Location/Qualifiers
1..2253
/organism="unidentified"
/db_xref="taxon:32644"
90..1475
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB58915.1"
/db_xref="GI:6090180"
/translation="NAPVAVWAALAVGLELMAAAHALPAQVAFTPYAPPGSGTCRLRE
YVDQAQCCSKCSPQOHAKVFCTXTSDVCDSCEDSTYTQLWNWVPECLSGSRCS
DQVQACTREQNRICRPGWYCALSKQEGRCAPLKRPGFGVARGPTETSDV
CRPCAPGTFSTNTSDICRPHQICNVVAIPGNAESGTDGFPALPVGLIVGTALGLII
PVSTRQHTQPTPEPTAPSTFLPLMPGSPPAEGSTGDFALPVGLIVGTALGLII
GVNVCVIMTQVKKKPLCLQREAKVPHLPADKARGTQGPQQHLLITAPSSSSLESS
ASALDRAPTRNOPQAPGVEASGAGEARASTGSSDSPGCHGTQVNVTCIVNVCSSD
HSSCQSSOASSTMGDTDSPPSPKDEQVPFSKECAFRSQLETPETLLGSTEKPLP
LGVPDAGMKPS"
BASE COUNT 440 a 709 c 698 g 406 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2253;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590
RESULT 6
A26415 2339 bp DNA linear PAT 26-APR-1995
LOCUS
DEFINITION cDNA fragment for (75kd TNF-BP) tumor necrosis factor binding
protein from patent EP0417563.
ACCESSION A26415

A26415.1 GI:904970
synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 2339)
AUTHORS Brockhaus,M., Dembic,Z., Gentz,R., Lesslauer,W., Loetscher,H. and
Schlaeger,E.J.
TITLE TNF-binding proteins
JOURNAL Patent: EP 0417563-A 27 20-MAR-1991;
F. HOFFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
1..2339
/organism="synthetic construct"
/db_xref="taxon:32630"
<1..1179
/codon_start=1
/translation_table=11
/product="75kd TNF-BP"
/protein_id="CAA01806.1"
/db_xref="GI:904971"
/translation="SDSVCDSCEDSTYTQLWNWVPECLSGSRCSQDVETQACTRQ
NRICTRPGWYCALSKQEGRCAPLKRPGFGVARGPTETSDVCKPCAPGTFST
TSSTDICRPHQICNVVAIPGNAESGTDGFPALPVGLIVGTALGLIIIGVWNCVIMTQV
PEPTAPSTFLPLMPGSPPAEGSTGDFALPVGLIVGTALGLIIIGVWNCVIMTQV
KKPLCLQREAKVPHLPADKARGTQGPQQHLLITAPSSSSLESSASALDRAPTRN
QPOAPGVEASGAGEARASTGSSDSPGCHGTQVNVTCIVNVCSSSDHSSCQSSOAS
TMGDTDSPPSPKDEQVPFSKECAFRSQLETPETLLGSTEKPLPLGVPDAGMKPS"
BASE COUNT 494 a 720 c 685 g 440 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 2339;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1274 AGGACTCTGAGGCTCTTTCT 1293
RESULT 7
HUMTNFR11 2394 bp mRNA linear PRI 03-SEP-1994
LOCUS Human tumor necrosis factor receptor II (TNFR11) mRNA, complete
DEFINITION cds
ACCESSION M55994 M38549
VERSION M55994.1 GI:339757
KEYWORDS glycoprotein; nerve growth factor receptor related; transmembrane
protein; tumor necrosis factor receptor; tumor necrosis factor
receptor II.
SOURCE Human histiocytic lymphoma cell line U937, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2394)
AUTHORS Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W.,
Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L.
TITLE A second tumor necrosis factor receptor gene product can shed a
naturally occurring tumor necrosis factor inhibitor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (21), 8331-8335 (1990)
MEDLINE 91045991
PUBMED 2172983
FEATURES Location/Qualifiers
1..2394
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/cell_type="histiocytic lymphoma"
1..2394
/gene="TNFR11"
93..1478
/gene="TNFR11"

/note="603. .611 and 669. .677 glycosylation site: 861. .947
transmembrane domain: 948. .1478 cytoplasmic domain;
159,860 extracellular domain"
/codon_start=1
/evidence=experimental
/product="tumor necrosis factor receptor"
/protein_id="AAA36755.1"
/db_xref="GI:339758"
/translation="MAPVAVMAALAVGLELWAAHAALPAQVAFTPYAPPGSTCLRRE
YDQVTAQCCSKSPGQHAQVCTKTSDTVCDSCEDSTYTQLMNWPBCLSCGRCS
DQVTAQCTREQNRICTRCPGWYCALSKQEGCLCAPKRCRPGFVGARPGTETSDV
CKCAPGTSTNTSDICRPHQICNVVAIPGNASMDAVCTSTPTSRMAPGAVHLPO
PVSTRQHTOPTPEPSTAPSTFLLPMGSPPAEGSTGDFALPGLIVGVTALGLLI
GVNVCYIMTVKKKPKLCLOREAKVPHLPADKARCTGQPEQOHLITAPSSSSSLESS
ASALDRAPTRNQPAQPGVEASGAEARASTGSSDSSPGGHTQVNTCIVNVCSSD
HSSQSSASSTMGTDSPSEPKDEQVFPFKRECAFRSQLETPETLLGSTEARPLP
LGVPDAGMKPS"
93. .158
/gene="TNFR1"
/note="putative"
159. .1475
/gene="TNFR1"
/product="tumor necrosis factor receptor"
/note="putative"
BASE COUNT 484 a 743 c 739 g 428 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 2394;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGACTCTGAGGCTCTTCT 20
|||||
Db 1574 AGGACTCTGAGGCTCTTCT 1593
RESULT 8
HSTNFR2S10 2613 bp DNA linear PRI 31-JUL-1996
LOCUS Human tumor necrosis factor receptor 2 (TNFR2) gene, exon 10 and
complete cds.
U52165.1 GI:1469539
1 of 10
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2613)
Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
Lepaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and
Brodeur,G.M.
TITLE Physical mapping and genomic structure of the human TNFR2 gene
JOURNAL Genomics 35 (1), 94-100 (1996)
MEDLINE 96299745
PUBMED 8661109
REFERENCE 2 (bases 1 to 2613)
Beltinger,C.P., White,P.S., Maris,J.M., Sulman,E.P., Jensen,S.J.,
Lepaslier,D., Stallard,B.J., Goeddel,D.V., de Sauvage,F.J. and
Brodeur,G.M.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-1996) Christian P. Beltinger, Division of
Oncology, ARC Rm. 902 D, Children's Hospital of Philadelphia, 324
South 34th Street, Philadelphia, PA 19104-4318, USA
FEATURES
source
1. .2613
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="lp36.2"
join(U52156.1:1. .167,U52157.1:7. .106,U52158.1:114. .242,
U52159.1:7. .156,U52160.1:7. .100,U52161.1:95. .330,
U52162.1:83. .160,U52163.1:7. .41,U52164.1:7. .211,125. .405)
/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAC50622.1"
/db_xref="GI:1469541"
/translation="MAPVAVMAALAVGLELWAAHAALPAQVAFTPYAPPGSTCLRRE
YDQVTAQCCSKSPGQHAQVCTKTSDTVCDSCEDSTYTQLMNWPBCLSCGRCS
DQVTAQCTREQNRICTRCPGWYCALSKQEGCLCAPKRCRPGFVGARPGTETSDV
CKCAPGTSTNTSDICRPHQICNVVAIPGNASMDAVCTSTPTSRMAPGAVHLPO
PVSTRQHTOPTPEPSTAPSTFLLPMGSPPAEGSTGDFALPGLIVGVTALGLLI
GVNVCYIMTVKKKPKLCLOREAKVPHLPADKARCTGQPEQOHLITAPSSSSSLESS
ASALDRAPTRNQPAQPGVEASGAEARASTGSSDSSPGGHTQVNTCIVNVCSSD
HSSQSSQASSTMGTDSPSEPKDEQVFPFKRECAFRSQLETPETLLGSTBEKPLP
LGVPDAGMKPS"
join(U52157.1:7. .112,U52158.1:1. .248,U52159.1:1. .200,
U52160.1:1. .106,U52161.1:1. .336,U52162.1:1. .218,
U52163.1:1. .58,U52164.1:1. .234,1. .2613)
/gene="TNFR2"
<1. .124
/gene="TNFR2"
/number=9
125. .2613
/gene="TNFR2"
/number=10
BASE COUNT 553 a 750 c 742 g 568 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 2613;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGACTCTGAGGCTCTTCT 20
|||||
Db 501 AGGACTCTGAGGCTCTTCT 520
RESULT 9
G26865
LOCUS human STS SHGC-31494, sequence tagged site.
DEFINITION G26865
ACCESSION G26865
VERSION G26865.1 GI:1375115
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3380)
Myers,R.M.
REFERENCE 1
AUTHORS Myers,R.M.
JOURNAL Unpublished (1995)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CCCACACCTAGGACTCTGA
Primer B: CACAGAGATCAGGACTTGC
STS size: 201
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30

U52162.1:83. .160,U52163.1:7. .41,U52164.1:7. .211,125. .2613)
/product="tumor necrosis factor receptor"
join(U52156.1:90. .167,U52157.1:7. .106,U52158.1:114. .242,
U52159.1:7. .156,U52160.1:7. .100,U52161.1:95. .330,
U52162.1:83. .160,U52163.1:7. .41,U52164.1:7. .211,125. .405)
/codon_start=1
/product="tumor necrosis factor receptor"
/protein_id="AAC50622.1"
/db_xref="GI:1469541"
/translation="MAPVAVMAALAVGLELWAAHAALPAQVAFTPYAPPGSTCLRRE
YDQVTAQCCSKSPGQHAQVCTKTSDTVCDSCEDSTYTQLMNWPBCLSCGRCS
DQVTAQCTREQNRICTRCPGWYCALSKQEGCLCAPKRCRPGFVGARPGTETSDV
CKCAPGTSTNTSDICRPHQICNVVAIPGNASMDAVCTSTPTSRMAPGAVHLPO
PVSTRQHTOPTPEPSTAPSTFLLPMGSPPAEGSTGDFALPGLIVGVTALGLLI
GVNVCYIMTVKKKPKLCLOREAKVPHLPADKARCTGQPEQOHLITAPSSSSSLESS
ASALDRAPTRNQPAQPGVEASGAEARASTGSSDSSPGGHTQVNTCIVNVCSSD
HSSQSSQASSTMGTDSPSEPKDEQVFPFKRECAFRSQLETPETLLGSTBEKPLP
LGVPDAGMKPS"
join(U52157.1:7. .112,U52158.1:1. .248,U52159.1:1. .200,
U52160.1:1. .106,U52161.1:1. .336,U52162.1:1. .218,
U52163.1:1. .58,U52164.1:1. .234,1. .2613)
/gene="TNFR2"
<1. .124
/gene="TNFR2"
/number=9
125. .2613
/gene="TNFR2"
/number=10
BASE COUNT 553 a 750 c 742 g 568 t
ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 2613;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AGGACTCTGAGGCTCTTCT 20
|||||
Db 501 AGGACTCTGAGGCTCTTCT 520
RESULT 9
G26865
LOCUS human STS SHGC-31494, sequence tagged site.
DEFINITION G26865
ACCESSION G26865
VERSION G26865.1 GI:1375115
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3380)
Myers,R.M.
REFERENCE 1
AUTHORS Myers,R.M.
JOURNAL Unpublished (1995)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CCCACACCTAGGACTCTGA
Primer B: CACAGAGATCAGGACTTGC
STS size: 201
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:

Template: 25 ng
each 1 uM
Primer: each 200 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul

Buffer:

MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from M32315
-- Washington University/Merck EST sequence.

FEATURES
source

Location/Qualifiers
1..3380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="1"

STS

primer_bind 1561..1761
primer_bind 1561..1580
complement(1741..1761)

BASE COUNT 703 a 1029 c 1004 g 644 t

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 3380;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGACTCTGAGGCTCTTTCT 20
|||||

Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 10

S63368

LOCUS S63368 3492 bp mRNA linear PRI 06-MAR-2001
DEFINITION Homo sapiens tumor necrosis factor receptor mRNA, partial cds.
ACCESSION S63368
VERSION S63368.1 GI:235648

SOURCE

human

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3492)

Dembic, Z., Loetscher, H., Gubler, U., Pan, Y. C., Lahm, H. W., Gentz, R.,

Brockhaus, M. and Lesslauer, W.

Two human TNF receptors have similar extracellular, but distinct

intracellular, domain sequences

Cytokine 2 (4), 231-237 (1990)

JOURNAL

MEDLINE

PUBMED

1966549

GenBank staff at the National Library of Medicine created this

entry [NCBI gibbsq 63368] from the original journal article.

This sequence comes from Figure 1.

Location/Qualifiers

1..3492

/organism="Homo sapiens"

/db_xref="taxon:9606"

<1..1278

/note="75-kDa; This sequence comes from Figure 1; TNF

receptor"

/codon_start=1

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/protein_id="AA019824.2"

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STYQLWNWPECLSGCRSDQVETQACTREQNRICTRPGWYCAUSKQEGCRICA

PLRKQRPVGPRTSDVCKPCAPGTFTNTSSDTCIRPHQTCNNVAIPGNASM

DAVCTSTSPTRSMAGVHLPPQVSTRSQHTQTPSTPSTFLLPMGPSVPAEGS

TGDFALPVGLIIVGVTALGLLIIGVNVVIMTOVKKKPLCLOREAKVPHLPADKARGTO
GPEQHLITAPSSSSSSLESSASALDRRAPTRNQOPQVGEASGAGARASTGSSDS
SPGQHGTVNVTCTIVNVSSSDSHSQCSQASSTMGDTDSSPSPKDEQVPFSKEEC
AFRSQLETPELLGSTEKPLPLGVPDAGMKPS"

BASE COUNT 757 a 1031 c 1006 g 698 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGACTCTGAGGCTCTTTCT 20
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Db 1374 AGGACTCTGAGGCTCTTTCT 1393

RESULT 11

AX333705

LOCUS

DEFINITION

Sequence 4214 from Patent WO0194629.

ACCESSION

AX333705

VERSION

AX333705.1

GI:18124424

KEYWORDS

human.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,

Horrigan, S., Soppet, D. R. and Weaver, Z.

Cancer gene determination and therapeutic screening using signature

gene sets

Patent: WO 0194629-A 4214 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

781 a 1098 c 1086 g 718 t

BASE COUNT

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGACTCTGAGGCTCTTTCT 20
|||||

Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 12

AX348016

LOCUS

DEFINITION

Sequence 49 from Patent EP1172444.

ACCESSION

AX348016

VERSION

AX348016.1

GI:18614126

KEYWORDS

human.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1

Schreiber, S., Hampe, J. and Mascheretti, S.

Diagnostic use of polymorphisms in the gene coding for the tnfr

receptor II and method for detecting non-responders to anti-tnf

therapy

Patent: EP 1172444-A 49 16-JAN-2002;

Conaris Research Institute GmbH (DE)

Location/Qualifiers

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/organism="Homo sapiens"

/db_xref="taxon:9606"

90..1475

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156
mat_peptide 781 a 1098 c 1086 g 718 t
BASE COUNT
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 13
AX348018
LOCUS AX348018 3683 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 51 from Patent EP1172444.
ACCESSION AX348018
VERSION AX348018.1 GI:18614128
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Schreiber, S., Hampe, J., and Mascheretti, S.
TITLE Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
JOURNAL Patent: EP 1172444-A 51 16-JAN-2002;
Conaris Research Institute GmbH (DE)
FEATURES
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1..3683
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90..1475
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156
mat_peptide 780 a 1098 c 1088 g 717 t
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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 15
HUMNFR
LOCUS HUMNFR 3683 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION M32315
VERSION M32315.1 GI:189185
KEYWORDS c-myc proto-oncogene; necrosis factor receptor.
SOURCE Homo sapiens lung CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3683)
AUTHORS Smith, C.A., Davis, T., Anderson, D., Solam, L., Beckmann, M.P.,
Jerzy, R., Dower, S.K., Cosman, D., and Goodwin, R.G.
TITLE A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins
JOURNAL Science 248 (4958), 1019-1023 (1990)
MEDLINE 90260639
PUBMED 2160731
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by C.A.Smith, 30-MAR-1990, for release after publication.
FEATURES
Location/Qualifiers
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RESULT 14
AX348020
LOCUS AX348020 3683 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 53 from Patent EP1172444.
ACCESSION AX348020
VERSION AX348020.1 GI:18614130
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Schreiber, S., Hampe, J., and Mascheretti, S.
TITLE Diagnostic use of polymorphisms in the gene coding for the tnfr
receptor II and method for detecting non-responders to anti-tnf
therapy
JOURNAL Patent: EP 1172444-A 53 16-JAN-2002;
Conaris Research Institute GmbH (DE)
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Source
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CKPCAPCTFSNTTSDTICRPHQICNVVAIPGNASMDVACTSTSPTRSMAPGAVHLPO
PVSTRSOHTOPTPEPSTAPSTSFLLPMGSPPAEGSTGDFALPVGLIVGTALGLLII
GVVNCVINTQVKKPKLCLOREAKVPHLPADKARGTQGPQQHLLITAPSSSSSSLESS
ASALDRRAPTRNQPAQGVASGAGEARASTGSDSPGGHGTVQNVTCIVNVCSSD
HSSQCSSQASSTMGDTSSPSPKDEQVPFSKECAFRSQLETPTLLGSTEKPLP
LGVPDAGMKPS"
156
mat_peptide 780 a 1098 c 1088 g 717 t
BASE COUNT
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3683;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTTCT 20
|||||
Db 1571 AGGACTCTGAGGCTCTTTCT 1590

RESULT 15
HUMNFR
LOCUS HUMNFR 3683 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human tumor necrosis factor receptor mRNA, complete cds.
ACCESSION M32315
VERSION M32315.1 GI:189185
KEYWORDS c-myc proto-oncogene; necrosis factor receptor.
SOURCE Homo sapiens lung CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 3683)
AUTHORS Smith, C.A., Davis, T., Anderson, D., Solam, L., Beckmann, M.P.,
Jerzy, R., Dower, S.K., Cosman, D., and Goodwin, R.G.
TITLE A receptor for tumor necrosis factor defines an unusual family of
cellular and viral proteins
JOURNAL Science 248 (4958), 1019-1023 (1990)
MEDLINE 90260639
PUBMED 2160731
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted
by C.A.Smith, 30-MAR-1990, for release after publication.
FEATURES
Location/Qualifiers
```


GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 4.80891 Seconds
(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937A-4

Perfect score: 20

Sequence: 1 aggaactctgaggtcttctt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAA49210	Human tumour necro
2	20	100.0	201	AAI12093	Human biallelic po
3	20	100.0	1640	AAQ10990	Partial sequence o
4	20	100.0	1641	AAQ49931	TNF-R CDNA. Homo
5	20	100.0	1641	AAQ45224	Sequence encoding
6	20	100.0	2339	AAQ10956	Encodes human 75kD
7	20	100.0	2339	AAQ209171	Human tumour necro
8	20	100.0	2339	AAH48860	Human TNFRP-associ
9	20	100.0	2393	AAQ10907	40kD TNF inhibitor

10	20	100.0	2394	22	AAC83951	Human 40 kDa TNF 1
11	20	100.0	2613	21	AAA49207	Human tumour necro
12	20	100.0	3683	24	ABK83997	Human cDNA differe
13	20	100.0	3683	24	ABL65877	Lung cancer relate
14	20	100.0	3683	24	ABK33465	Human TNF receptor
15	20	100.0	3683	24	ABK33466	Human TNF receptor
16	20	100.0	3683	24	ABK33467	Human TNF receptor
17	19	95.0	25	24	ABK33459	Human TNF-receptor
18	18.4	92.0	2224	16	AAQ89544	p75 Tumour Necrosi
19	17	85.0	485	21	AAQ03830	Human secreted pro
20	17	85.0	1280	17	AAT33354	Human Ich-2 protei
C 21	16.8	84.0	322	23	ABV06635	Human prostate exp
C 22	16.8	84.0	407	23	ABV36584	Human prostate exp
C 23	16.8	84.0	480	22	ABA52150	Human prostate exp
C 24	16.8	84.0	480	22	ABA21957	Human foetal liver
C 25	16.8	84.0	480	22	AAK00430	Probe #423 for gen
C 26	16.8	84.0	480	22	AAK25873	Human brain expres
C 27	16.8	84.0	480	22	AAI10503	Human bone marrow
C 28	16.8	84.0	480	22	AAI31757	Probe #436 for gen
C 29	16.8	84.0	480	22	AAI00436	Probe #443 used to
C 30	16.8	84.0	480	22	ABS00456	Probe #427 used to
C 31	16.8	84.0	580	24	ABL83157	Human genome-deriv
C 32	16.8	84.0	966	22	ABA64903	Human ovarian canc
C 33	16.8	84.0	966	22	ABA64784	Human breast cell
C 34	16.8	84.0	966	22	ABA31902	Human foetal liver
C 35	16.8	84.0	966	22	AAK13216	Probe #10368 for g
C 36	16.8	84.0	966	22	AAK38947	Human brain expres
C 37	16.8	84.0	966	22	AAI19757	Human bone marrow
C 38	16.8	84.0	966	22	AAI44953	Probe #9690 for ge
C 39	16.8	84.0	966	22	AAI05474	Probe #13639 used
C 40	16.8	84.0	966	24	ABS13031	Probe #5465 used t
C 41	16.8	84.0	1086	22	ABA46796	Human genome-deriv
C 42	16.8	84.0	1086	22	ABA47311	Human breast cell
C 43	16.8	84.0	1086	22	ABA64676	Human foetal liver
C 44	16.8	84.0	1086	22	ABA65196	Human foetal liver
C 45	16.8	84.0	1086	22	ABA31800	Probe #10266 for g

ALIGNMENTS

RESULT 1
AAA49210
ID AAA49210 standard; DNA; 20 BP.
XX
AC AAA49210;
XX
XX 22-NOV-2000 (first entry)
XX
XX Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-7.

DE Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-7.
XX
KW Human: tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW osteoporosis; PCR primer; ss.
XX
OS Homo sapiens.

XX
XX WO2000032826-A1.
XX
PD 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US28403.
XX
XX 30-NOV-1998; 98US-0110268.
PR
XX (UYDR-) UNIV DREXEL.

PA Spotilla LD;

XX WPI; 2000-412362/35.

XX Identifying individuals at risk of developing osteoporosis comprises

PT assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
PT in a DNA sample from an individual -

XX Example 3; Page 12; 21pp; English.

XX The present sequence is a PCR primer for the three polymorphic sites

CC within exon 10 of the human tumour necrosis factor alpha receptor 2

CC (THFR2) gene. By determining the genotype of an individual it is possible

CC to identify those at risk of osteoporosis, which is characterised by low

CC bone density and fragile bones, later in life. Those at greatest risk are

CC those who possess allele 1, which is the rarest allele. This is

CC particularly useful as many cases of osteoporosis go undetected at

CC present. The primer can be used to determine an individual's genotype,

CC and, therefore, their risk of osteoporosis.

XX Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 other;

SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 other;

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Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGGACTCTGAGGCTCTTTCT 20

RESULT 2

AAAX12093

ID AAX12093 standard; DNA; 201 BP.

AC AAX12093;

DT 30-MAR-1999 (first entry)

XX Human biallelic polymorphic DNA fragment M32315b.

DE Polymorphism: biallelic; human; forensic; paternity testing; disease;

KW detection; phenotypic typing; characteristic; infection; hereditary;

KW autoimmune disease; cancer; inflammation; drug; therapy; medicament;

KW treatment; marker; ss.

XX Homo sapiens.

XX WO9820165-A2.

XX 14-MAY-1998.

XX 05-NOV-1997; 97WO-US20313.

XX 06-NOV-1996; 96US-0030455.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX Hudson T, Lander ES, Wang D;

XX WPI; 1998-286974/25.

XX New isolated nucleic acid segments from the human genome - used for

PT determining polymorphic forms for use in e.g. forensics, paternity

PT testing or phenotypic typing for disease

XX Claim 1; Page 219; 310pp; English.

XX AAX10269-X12937 are human DNA fragments which contain biallelic

CC polymorphic markers which have been isolated using the primers

CC represented in AAX09121-X10268. The base occupying the polymorphic site

CC is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments

CC can be used in methods for determining polymorphic forms in an individual

CC for use in e.g. forensics, paternity testing or for phenotypic typing for

CC diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan

CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,

CC familial hypercholesterolemia, polycystic kidney disease, hereditary

CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary

CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos

CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,

CC autoimmune diseases, inflammation, cancer, diseases of the nervous

CC system, infection by pathogenic microorganisms, and characteristics such

CC as longevity, appearance (e.g. baldness, obesity), strength, speed,

CC endurance, fertility, and susceptibility or receptivity to particular

CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid

CC segments can also be used to produce medicaments for the treatment or

CC prophylaxis of such diseases.

XX Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

SQ Sequence 201 BP; 32 A; 65 C; 62 G; 41 T; 1 other;

Query Match 100.0%; Score 20; DB 19; Length 201;

Best Local Similarity 100.0%; Pred. No. 4.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGGACTCTGAGGCTCTTTCT 20

Db 11 AGGACTCTGAGGCTCTTTCT 30

RESULT 3

AAQ10990

ID AAQ10990 standard; cDNA to mRNA; 1640 BP.

XX AAQ10990;

XX 24-MAY-1991 (first entry)

DT Partial sequence of hTNF-R clone 1.

XX Tumour necrosis factor receptor; immune response; inflammation;

KW cachexia; septic shock; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 88..1473

FT mat_peptide 154..1470

FT sig_peptide 88..153

FT /*tag= a

FT /*tag= b

FT /*tag= c

XX EP418014-A.

XX 20-MAR-1991.

XX 10-SEP-1990; 90EP-0309875.

XX 10-MAY-1990; 90US-0523635.

XX 11-SEP-1989; 89US-0405370.

XX 13-OCT-1989; 89US-0421417.

XX (IMMU-) IMMUNEX CORP.

XX Smith CA, Goodwin RG, Beckmann PM;

XX WPI; 1991-082230/12.

XX P-PSDB; AAR11141.

XX New tumour necrosis factor -alpha and -beta receptors - and DNA

PT encoding these used to regulate immune responses in treatment of

PT cachexia, septic shock or side-effects of cytokine therapy.

XX Claim 1; Fig 2; 41pp; English.

XX The sequence was obtd. from a clone isolated from library prepd.

CC from a human fibroblast cell line, WI-26 VA4 (ATCC CCL 95.1).

CC The clone is deposited as Accession No. 68088 under the name

CC PCAV/NOT-TNF-R. The DNA can be truncated to produce sequences which

CC express soluble receptor comprising residues 1-235, 1-185 or 1-163

CC of the protein.

CC See also AAQ10991.

```

SQ Sequence 1640 BP; 328 A; 543 C; 502 G; 267 T; 0 other:
Query Match          100.0%; Score 20; DB 12; Length 1640;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1569 AGGACTCTGAGGCTCTTTCT 1588

RESULT 4
AAQ49931
ID AAQ49931 standard; cDNA to mRNA; 1641 BP.
XX
AC AAQ49931;
XX
DT 29-APR-1994 (first entry)
XX
DE TNF-R cDNA.
XX
KW Human: tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;
KW rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KW pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KW graft versus host disease; sepsis; inflammation; allergy;
KW autoimmune dysfunction; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /*tag= a
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FT sig_peptide 88..153
FT /*tag= b
FT mat_peptide 154..1470
FT /*tag= c
FT
FT
XX
PN W09319777-A.
XX
PD 14-OCT-1993.
XX
PE 26-MAR-1993; 93WO-US02938.
XX
PR 30-MAR-1992; 92US-0860710.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Smith CA;
XX
PI WPI: 1993-336592/42.
XX
DR P-PSDB; AAR42058.
XX
PT New fusion protein tumour necrosis factor and human interleukin-1
PT receptor - useful in therapy, diagnosis and assays of e.g.
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX
PS Disclosure; Fig 2; 85pp; English.
XX
CC The sequences given in AAQ49931-32 encode human tumour necrosis factor
CC receptor (TNF-R) and the sequences in AAQ49933-34 encode human
CC interleukin-1 receptor (IL-1R). These sequences were used in the
CC production of a fusion protein which conformed to one of the
CC formulae:
CC TNF-R-linker-TNF-R-linker-IL-1R
CC IL-1R-linker-TNF-R-linker-TNF-R or
CC TNF-R-linker-TNF-R
CC The linker may comprise 5-100 amino acids selected from Gly, Asp,
CC Ser, Thr and Ala. These linkers separate the individual moieties
CC by such a distance that each component of the fusion protein is
CC capable of folding into the secondary or tertiary structure required
CC for its biological activity. These fusion proteins may be used in

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CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC particularly in conditions in which both TNF and IL-1 play a causative
CC role. They may be used to treat cachexia, rheumatoid arthritis,
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC cerebral malaria, allograft and xenograft rejection in graft versus
CC host disease, sepsis, septic shock, inflammation, allergies and
CC autoimmune dysfunctions.
XX
SQ Sequence 1641 BP; 328 A; 544 C; 502 G; 267 T; 0 other:
Query Match          100.0%; Score 20; DB 14; Length 1641;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGACTCTGAGGCTCTTTCT 20
   |||||||
DB 1569 AGGACTCTGAGGCTCTTTCT 1588

RESULT 5
AAQ45224
ID AAQ45224 standard; cDNA; 1641 BP.
XX
AC AAQ45224;
XX
DT 07-OCT-1994 (first entry)
XX
DE Sequence encoding human tumour necrosis factor receptor type I
DE (TNFRI).
XX
KW Tumour necrosis factor receptor; type I; TNFRI; arthritis therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 154..1470
FT /*tag= a
FT sig_peptide 88..153
FT /*tag= b
FT
FT
XX
PN W09406476-A.
XX
PD 31-MAR-1994.
XX
PE 14-SEP-1993; 93WO-US08666.
XX
PR 15-SEP-1992; 92US-0946236.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Jacobs CA, Smith CA;
XX
PI WPI: 1994-118172/14.
XX
DR P-PSDB; AAR51002.
XX
PT Treating TNF mediated inflammatory diseases with TNF antagonist -
PT esp. soluble form of TNF receptor, opt. as fusion protein with
PT human immunoglobulin Fc region, esp. for treating arthritis
XX
PS Disclosure; Page 28-30; 47pp; English.
XX
CC AAQ45224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
CC cell line WI-26 VA4. The mature full-length TNFRI is a glycoprotein
CC having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
CC TNFRI was described in Smith et al., Science 248:1019,1990. Clone 1
CC is contained in expression vector pCAV/NOT-TNFR (ATCC 68088). The
CC preferred TNFRs of the present invention are soluble forms of TNFRI
CC and TNFRII having at least 20 AAs. Soluble TNFR constructs are
CC devoid of a transmembrane region but retain the ability to bind TNF.
CC Examples of soluble TNFRs are hTNFRIdelta235, hTNFRIdelta185 and
CC hTNFRIdelta163 which encode respectively AAs 1-235, 1-185 and 1-163
CC of AAR51002. An equivalent soluble TNFR is hTNFRIdelta163 wherein x
CC is selected from any one of AAs 163-235 of AAR51002.

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XX Sequence 1641 BP: 328 A; 526 C; 520 G; 267 T; 0 other:
SO
Query Match 100.0%; Score 20; DB 15; Length 1641;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGGCTCTTCT 20
    |||
DB 1569 AGGACTCTGAGGCTCTTCT 1568

RESULT 6
AAO10956
ID AAO10956 standard; DNA: 2339 BP.
XX
AC AAO10956;
XX
XX 24-MAY-1991 (first entry)
XX
DE Encodes human 75KD TNF-binding protein.
XX
XX Tumour Necrosis Factor; binding proteins; septic shock;
XX autoimmune glomerulonephritis; lymphokine; cytokine.
XX
XX Key Location/Qualifiers
XX CDS 1..1179
XX FT /*tag= a
XX FT /product= 75KD TNF-BP
XX
XX EPA17563-A.
XX
XX 20-MAR-1991.
XX
XX 31-AUG-1990; 90EP-0116707.
XX
XX PF 20-APR-1990; 90CH-0001347.
XX PR 12-SEP-1989; 89CH-0003319.
XX PR 08-MAR-1990; 90CH-0000746.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
XX Schlaeger EJ;
XX
XX WPI: 1991-081851/12.
XX DR P-PSDB: AAR1605.
XX
XX Insoluble tumour necrosis factor binding proteins - and DNA
XX encoding them, useful in pharmaceutical prods. and for antibody
XX prodn.
XX
XX Claim 4; Fig 1: 26pp; German.
XX
XX Partial amino acid sequences were determined for the 55 and 75KD
XX TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
XX synthesised based on these partial sequences. The primers were used
XX to produce a cDNA fragment for use as a probe to screen a human
XX placental cDNA bank constructed in lambda gt11. Positive clones were
XX identified and sequenced. Repeated sequencing showed a discrepancy
XX at position 7 such that the third codon encodes either Thr or Ser.
XX CC DNA constructs comprising the TNF-BP coding sequence may also
XX contain a fragment encoding a human Ig domain. Recombinant
XX constructs are used to transform cells to confer improved TNF-
XX binding properties.
XX See also AAO10955.
XX
XX Sequence 2339 BP: 494 A; 720 C; 685 G; 439 T; 1 other:
SO
Query Match 100.0%; Score 20; DB 12; Length 2339;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 AGGACTCTGAGGCTCTTCT 20
    |||
DB 1274 AGGACTCTGAGGCTCTTCT 1293

RESULT 7
AAZ09171
ID AAZ09171 standard; cDNA: 2339 BP.
XX
AC AAZ09171;
XX
XX 18-OCT-1999 (first entry)
XX
DE Human tumour necrosis factor binding protein cDNA fragment.
XX
XX Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
XX anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
XX autoimmune glomerulonephritis; cerebral malaria; immune response;
XX antagonist; diagnosis; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..1179
XX FT /*tag= a
XX FT /product= "TNF binding protein"
XX FT /note= "Partial sequence, no start codon given"
XX
XX EP939121-A2.
XX
XX 01-SEP-1999.
XX
XX 31-AUG-1990; 90EP-0116707.
XX
XX PF 20-APR-1990; 90CH-0001347.
XX PR 12-SEP-1989; 89CH-0003319.
XX PR 08-MAR-1990; 90CH-0000746.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
XX PI Schlaeger EJ;
XX
XX WPI: 1999-480840/41.
XX DR P-PSDB: AAY30935.
XX
XX New insoluble proteins, and fragments, that bind to tumor necrosis
XX factor, used to treat e.g. septic shock or cerebral malaria
XX
XX Claim 4a; Fig 4: 25pp; German.
XX
XX This invention describes novel homogeneous insoluble proteins (I),
XX their (in)soluble fragments (IIa) and their salts that can bind tumour
XX necrosis factor (TNF). The products of the invention have
XX anti-inflammatory and antimalarial activity. (I) and (IIa) are used (I)
XX to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
XX glomerulonephritis, cerebral malaria, immune responses and inflammation),
XX (II) to purify TNF, (III) to identify TNF (ant)agonists and (IV) for
XX diagnostic determination of TNF in body fluids. Antibodies raised against
XX (I) are used for affinity purification of (II). This sequence encodes
XX a tumour necrosis factor binding protein fragment described in the method
XX of the invention.
XX
XX Sequence 2339 BP: 494 A; 720 C; 685 G; 440 T; 0 other:
SO
Query Match 100.0%; Score 20; DB 20; Length 2339;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGGCTCTTCT 20
    |||
DB 1274 AGGACTCTGAGGCTCTTCT 1293

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RESULT 8
AAH48860
ID AAH48860 standard; DNA: 2339 BP.
XX
XX AAH48860;
AC
XX
XX 12-NOV-2001 (first entry)
DT
XX
XX Human TNFBP-associated DNA #2.
DE
XX
XX TNF: tumor necrosis factor binding protein; TNFBP; treatment:
KW insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
KW antiprotocoeal; treatment: meningococcal sepsis; cerebral malaria;
KW autoimmune glomerulonephritis; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 1..1179
FT /*tag= a
FT CDS /product= "TNFBP-associated protein"
FT
XX
XX EP1132471-A2.
XX
XX 12-SEP-2001.
PD
XX
XX 31-AUG-1990; 2001EP-0108117.
XX
XX 12-SEP-1989; 89CH-0003319.
XX 08-MAR-1990; 90CH-0000746.
XX 20-APR-1990; 90CH-0001347.
XX 31-AUG-1990; 90EP-0116707.
XX 31-AUG-1990; 99EP-0100703.
XX
XX (HOF ) HOFMANN LA ROCHE & CO AG F.
XX
XX Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;
PI Schlaeger E;
XX
XX WPI: 2001-559312/63.
XX
XX P-PSDB; AAB86818.
DR
XX
XX New homogeneous, insoluble proteins that bind tumor necrosis factor
PT (TNF), useful for treating TNF-mediated disorders, e.g. inflammation -
PT
XX
XX Claim 4a; Fig 4; 26pp; German.
PS
XX
XX This invention describes novel insoluble proteins (I), also their
CC (insoluble) fragments and pharmaceutically acceptable salts, able to bind
CC tumor necrosis factor (TNF) and in homogeneous form. The products of the
CC invention have antiinflammatory, immunosuppressive, antibacterial,
CC antiprotocoeal activity. (I), and related recombinant proteins, are used
CC to treat diseases mediated by TNF, e.g. shock in cases of meningococcal
CC sepsis; development of autoimmune glomerulonephritis and cerebral
CC malaria. Also (I), or antibodies specific for them, are used for
CC diagnostic determination of TNF in body fluids; for affinity purification
CC of TNF and for identifying (ant)agonists of TNF. This sequence encodes a
CC human TNF binding protein described in the method of the invention.
XX
XX
SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other:
Query Match 100.0%; Score 20; DB 22; Length 2339;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGACTCTGAGCCTCTTCT 20
Db 1274 AGGACTCTGAGCCTCTTCT 1293

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ID AAQ10907 standard; cDNA; 2393 BP.
XX
XX AAQ10907;
AC
XX
XX 13-MAY-1991 (first entry)
DT
XX
XX 40kd TNF inhibitor precursor gene in c40DK#6.
XX
XX Tumour necrosis factor; inhibitor; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 93..1478
FT CDS /*tag= a
FT
XX
XX AU9058976-A.
XX
XX 24-JAN-1991.
PD
XX
XX 16-JUL-1990; 90AU-0058976.
XX
XX 07-FEB-1990; 90US-0479661.
XX 18-JUL-1989; 89US-0381080.
XX 11-DEC-1989; 89US-0450329.
XX
XX (SYNE-) SYNERGEN INC.
XX
XX WPI: 1991-073847/11.
XX
XX P-PSDB; AAR11001.
DR
XX
XX Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT and -beta, useful as therapeutic agent.
PT
XX
XX Disclosure; Fig 39; 142pp; English.
PS
XX
XX The sequence encodes the entire 40 kD TNF inhibitor. The clone from
CC which the sequence was obt'd. was isolated from a cDNA library
CC prep'd. from RNA form U937 cells treated with PMA/PMA. The whole
CC gene can be inserted into expression vectors for prep'n. of TNF
CC inhibitor for use in the treatment of inflammatory and degenerative
CC diseases.
CC See also AAQ10878, AAQ10884 and AAQ10883.
XX
XX
SQ Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other:
Query Match 100.0%; Score 20; DB 12; Length 2393;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGACTCTGAGCCTCTTCT 20
Db 1573 AGGACTCTGAGCCTCTTCT 1592

```

RESULT 9
AAQ10907

```

RESULT 10
AAC83951
ID AAC83951 standard; DNA: 2394 BP.
XX
XX AAC83951;
AC
XX
XX 02-MAR-2001 (first entry)
DT
XX
XX Human 40 kDa TNF inhibitor precursor coding sequence.
XX
XX TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human; lymphotoxin; ss.
XX
XX Homo sapiens.
OS
XX
XX US6143866-A.
XX
XX 07-NOV-2000.
PD

```

PF	XX	19-JAN-1995:	95US-0375242.						
PR	XX	19-JUL-1990:	90US-0555274.						
PR	XX	09-JUL-1993:	93US-0090366.						
PR	XX	18-JUL-1989:	89US-0381080.						
PR	XX	11-DEC-1989:	89US-0450329.						
PR	XX	07-FEB-1990:	90US-0479661.						
PA	XX	(AMGE-) AMGEN INC.							
PI	XX	Squires C, Kling MW, Hale KK, Brewer MT, Thompson RC;							
PI	XX	Vanderslice RW, Vannice J, Kohno T;							
DR	XX	WPI: 2001-006443/01.							
DR	XX	P-PSDB: AAB37686.							
PT	XX	Novel 30 kDa tumor necrosis factor inhibitor analog comprising a							
PT	XX	non-native cysteine residue cross-linked with polyethylene glycol,							
PT	XX	useful for treating inflammatory and degenerative diseases mediated by							
PT	XX	TNF							
PS	XX	Example 12: Fig 39: 82pp: English.							
CC	XX	The present invention relates to Tumour Necrosis Factor (TNF) inhibitors							
CC	XX	(see AAB37676 and AAB37685), which have TNF inhibitory activity. The							
CC	XX	novel TNF inhibitors of the present invention are useful as therapeutic							
CC	XX	agents for inhibiting the activity of TNF and interleukin (IL-1), and							
CC	XX	for treating inflammatory and degenerative diseases mediated by TNF. The							
CC	XX	present sequence is the coding sequence for the precursor of 40 kDa TNF							
CC	XX	inhibitor. The 40 kDa TNF inhibitor can inhibit both TNF alpha and beta							
CC	XX	(lymphotoxin).							
SQ	XX	Sequence 2394 BP: 484 A; 743 C; 738 G; 428 T; 1 other;							
Query Match		100.0%: Score 20: DB 22: Length 2394:							
Best Local Similarity		100.0%: Pred. No. 5.4:							
Matches	20;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
UY		1 AGGACTCTGAGCCTCTTCT 20							
Db		1574 AGGACTCTGAGCCTCTTCT 1593							
RESULT 11									
AAA49207									
ID	AAA49207	standard; DNA; 2613 BP.							
AC	XX								
AC	XX	AAA49207;							
DT	XX	22-NOV-2000 (first entry)							
XX									
DE	XX	Human tumour necrosis factor alpha receptor 2 gene exon 10.							
XX									
KM	XX	Human: tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;							
KW	XX	osteoporosis; ds.							
OS	XX	Homo sapiens.							
XX									
XX									
key	XX	Location/Qualifiers							
PH	XX	1..2613							
CDS	XX	/tag= a							
FT	XX	/product= "TNFR2"							
FT	XX	/partial							
FT	XX	replace (593..A), (598..G), (620..T)							
FT	XX	/tag= b							
FT	XX	/label= allele_1							
FT	XX	replace (593..A), (598..T), (620..T)							
FT	XX	/tag= c							
FT	XX	/label= allele_2							
FT	XX	replace (593..G), (598..T), (620..C)							
FT	XX	/tag= d							
FT	XX	/label= allele_3							

FT	allele	replace (593,G), (598,T), (620,T)
FT		/tag=
FT		/label= allele_4
FT	allele	replace (593,A), (598,T), (620,C)
FT		/tag= f
FT		/label= allele_5
XX		
PN	MO200032826-A1.	
XX		
PD	08-JUN-2000.	
XX		
PF	30-NOV-1999:	99WO-US28403.
XX		
PR	30-NOV-1998:	98US-0110268.
XX		
PA	(UYDR-) UNIV DREXEL.	
XX		
XX	Spotila LD:	
DR	WPI: 2000-412362/35.	
XX		
PT	Identifying individuals at risk of developing osteoporosis comprises	
PT	assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene	
PT	in a DNA sample from an individual -	
XX		
PS	Claim 2: Page 17-18; 21pp; English.	
CC		
CC	The present sequence comprises exon 10 of the human tumour necrosis	
CC	factor alpha receptor 2 (TNFR2) gene. The sequence contains three	
CC	polymorphic sites. By determining the genotype of an individual it is	
CC	possible to identify those at risk of osteoporosis, which is	
CC	characterised by low bone density and fragile bones, later in life. Those	
CC	at greatest risk are those who possess allele 1, which is the rarest	
CC	allele. This is particularly useful as many cases of osteoporosis go	
CC	undetected at present.	
XX		
XX		
SQ	Sequence 2613 BP: 553 A: 750 C: 742 G: 568 T: 0 other:	
	Query Match	100.0%; Score 20: DB 21: Length 2613:
	Best Local Similarity	100.0%; Pred. No. 5.5;
	Matches 20: Conservative	0: Mismatches 0: Indels 0: Gaps 0:
QY	1 AGGACCTGAGGCTCTTCT 20	
DB	501 AGGACCTGAGGCTCTTCT 520	
	RESULT 12	
	ABR83997	
ID	ABR83997 standard: cDNA: 3683 BP.	
XX		
AC	ABR83997:	
XX		
DT	14-AUG-2002 (first entry)	
XX		
DE	Human cDNA differentially expressed in granulocytic cells #568.	
XX		
XX	Human: ss; granulocytic cell; DNA chip: bacterial infection;	
XX	viral infection; parasitic infection; protozoal infection;	
XX	fungal infection; sterile inflammatory disease; psoriasis;	
XX	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;	
XX	cardiac reperfusion injury; renal reperfusion injury; ARDS;	
XX	adult respiratory distress syndrome; inflammatory bowel disease;	
XX	Crohn's disease; ulcerative colitis; periodontal disease;	
XX	granulocyte activation; chronic inflammation; allergy.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200228999-A2.	
XX		
PD	11-APR-2002.	
XX		
PF	03-OCT-2001: 2001WO-US30821.	

XX 03-OCT-2000; 2000US-237189P.
PR (GENE-) GENE LOCIC INC.
XX
XX Beazar-Barclay Y, Weissman SM, Yamaga S, Vockley J;
PI
XX
XX MPI: 2002-435328/46.
XX
XX
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PR diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
XX
XX Claim 1; SEQ ID NO 568; 114pp; English.
XX
XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC peritoneal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other:
SO
Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGACTGTGAGGCTTTCT 20
DB 1571 AGGACTGTGAGGCTTTCT 1590
IIIIIIIIIIIIIIIIIIIIII
RESULT 13
ABL65877
ID ABL65877 standard; DNA: 3683 BP.
XX
XX ABL65877:
AC
XX
XX 15-MAY-2002 (first entry)
DT
XX Lung cancer related gene sequence SEQ ID NO:4214.
DE

XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
XX Homo sapiens.
OS
XX
XX MO200194629-A2.
PN
XX
XX 13-DEC-2001.
PD
XX
XX
XX 30-MAY-2001; 2001WO-US10838.
PF
XX
XX 05-JUN-2000; 2000US-209473P.
PR
XX 05-JUN-2000; 2000US-209531P.
PR
XX 18-SEP-2000; 2000US-233133P.
PR
XX 18-SEP-2000; 2000US-233617P.
PR
XX 20-SEP-2000; 2000US-234009P.
PR
XX 20-SEP-2000; 2000US-234034P.
PR
XX 20-SEP-2000; 2000US-234052P.
PR
XX 22-SEP-2000; 2000US-234509P.
PR
XX 22-SEP-2000; 2000US-234567P.
PR
XX 25-SEP-2000; 2000US-234923P.
PR
XX 25-SEP-2000; 2000US-234924P.
PR
XX 25-SEP-2000; 2000US-235077P.
PR
XX 25-SEP-2000; 2000US-235082P.
PR
XX 25-SEP-2000; 2000US-235134P.
PR
XX 25-SEP-2000; 2000US-235280P.
PR
XX 26-SEP-2000; 2000US-235637P.
PR
XX 26-SEP-2000; 2000US-235638P.
PR
XX 27-SEP-2000; 2000US-235711P.
PR
XX 27-SEP-2000; 2000US-235720P.
PR
XX 27-SEP-2000; 2000US-235840P.
PR
XX 27-SEP-2000; 2000US-235863P.
PR
XX 28-SEP-2000; 2000US-236028P.
PR
XX 28-SEP-2000; 2000US-236032P.
PR
XX 28-SEP-2000; 2000US-236033P.
PR
XX 28-SEP-2000; 2000US-236034P.
PR
XX 28-SEP-2000; 2000US-236109P.
PR
XX 28-SEP-2000; 2000US-236111P.
PR
XX 29-SEP-2000; 2000US-236842P.
PR
XX 29-SEP-2000; 2000US-236891P.
PR
XX 02-OCT-2000; 2000US-237172P.
PR
XX 02-OCT-2000; 2000US-237173P.
PR
XX 02-OCT-2000; 2000US-237278P.
PR
XX 02-OCT-2000; 2000US-237294P.
PR
XX 02-OCT-2000; 2000US-237295P.
PR
XX 02-OCT-2000; 2000US-237316P.
PR
XX 03-OCT-2000; 2000US-237425P.
PR
XX 03-OCT-2000; 2000US-237598P.
PR
XX 03-OCT-2000; 2000US-237604P.
PR
XX 03-OCT-2000; 2000US-237606P.
PR
XX 03-OCT-2000; 2000US-237608P.
PR
XX 01-NOV-2000; 2000US-244867P.
PR
XX 01-NOV-2000; 2000US-245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
XX MPI: 2002-188264/24.
XX
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
XX
XX Claim 1; SEQ ID 4214; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophagel, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms' tumour.

SO Sequence 3683 BP: 781 A: 1098 C: 1086 G: 718 T: 0 other:

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGGCTCTTCT 20
|||||
DB 1571 AGGACTCTGAGGCTCTTCT 1590

RESULT 14

ABK33465
ID ABK33465 standard; DNA: 3683 BP.

AC ABK33465;

DT 23-APR-2002 (first entry)

DE Human TNF receptor II gene.

XX Human: anti-tumour necrosis factor receptor II; TNF receptor II;

KW Chromosome 1p36; Infliximab therapy; Crohn's disease; malignant disorder;

KW Inflammatory disorder; chronic disease; receptor; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 90..1475

FT /*tag= a

FT /product= "TNF receptor II"

FT sig_peptide 90..155

FT /*tag= b

FT mat_peptide 156..1472

FT /*tag= c

FT EP1172444-A1.

PN 16-JAN-2002.

PD 10-JUL-2000; 2000EP-0114786.

PE 10-JUL-2000; 2000EP-0114786.

PR 10-JUL-2000; 2000EP-0114786.

XX (CONA-) CONARIS RES INST GMBH.

XX Schreiber S, Hampe J, Mascheretti S;

XX WPI: 2002-156651/21.

DR P-PSDB: AAU75172.

XX Detecting non-responders to anti-human necrosis factor therapy,
PT comprises testing an individual for homozygosity for a single
PT nucleotide polymorphism in the gene coding for the tumour necrosis
PT factor receptor II -

XX Disclosure: Page 23-27; 45pp; English.

CC The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC Met196Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC infliximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC encodes for human TNF receptor II.

SO Sequence 3683 BP: 781 A: 1098 C: 1086 G: 718 T: 0 other:

Query Match 100.0%; Score 20; DB 24; Length 3683;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGGCTCTTCT 20
|||||
DB 1571 AGGACTCTGAGGCTCTTCT 1590

RESULT 15

ABK33466
ID ABK33466 standard; DNA: 3683 BP.

AC ABK33466;

DT 23-APR-2002 (first entry)

DE Human TNF receptor II gene with SNP in exon 2.

XX Human: anti-tumour necrosis factor receptor II; TNF receptor II; SNP;

KW Chromosome 1p36; Infliximab therapy; Crohn's disease; malignant disorder;

KW Inflammatory disorder; chronic disease; receptor; gene; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 90..1475

FT /*tag= a

FT /product= "TNF receptor II variant #1"

FT sig_peptide 90..155

FT /*tag= b

FT mat_peptide 156..1472

FT /*tag= c

FT variation replace (257, A)

FT /*tag= d

FT standard_name= "Single nucleotide polymorphism"

PN EP1172444-A1.

PD 16-JAN-2002.

PE 10-JUL-2000; 2000EP-0114786.

PR 10-JUL-2000; 2000EP-0114786.

XX (CONA-) CONARIS RES INST GMBH.

XX Schreiber S, Hampe J, Mascheretti S;

XX WPI: 2002-156651/21.

DR P-PSDB: AAU75173.

XX Detecting non-responders to anti-human necrosis factor therapy,
PT comprises testing an individual for homozygosity for a single
PT nucleotide polymorphism in the gene coding for the tumour necrosis
PT factor receptor II -

PS Claim 15; Page 29-33; 45pp; English.

XX
CC The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC A/C) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC Met196Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC Infliximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC represents the human TNF receptor II gene containing the SNP in exon 2.
XX

SQ Sequence 3683 BP; 780 A; 1098 C; 1087 G; 718 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 3683;

Best Local Similarity 100.0%; Pred. No. 5.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTCTGAGGCTCTTCT 20

|||||

ub 1571 AGGACTCTGAGGCTCTTCT 1590

Search completed: December 5, 2002, 23:30:05
Job time : 9.80891 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 ; Search time 38.2783 Seconds
(without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937A-4
Perfect score: 20
Sequence: 1 agagctctgagctcttct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estcp1:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Prod. No., is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	150	10	AM176594 RC5-CT007
2	20	100.0	372	9	AA031826 zk14b1.r
3	20	100.0	760	13	B1161017 602865227
4	20	100.0	827	12	BF347834 602022970
5	20	100.0	845	13	B1160187 602864057
6	20	100.0	932	12	BC829828 602764119

c	7	20	100.0	1051	12	BF568409	BF568409 602184408
	8	20	100.0	1053	14	BO052282	BO052282 AGENCOURT
	9	20	100.0	1066	12	BF568708	BF568708 602184353
	10	20	100.0	1102	14	BM917316	BM917316 AGENCOURT
	11	20	100.0	2291	11	BC011844	BC011844 Homo sapi
	12	18.4	92.0	175	10	AM062603	AM062603 RC0-CT008
c	13	18.4	92.0	602	17	AC129979	AC129979 Pan trogl
c	14	18	90.0	562	17	AZ803826	AZ803826 2M0064J19
c	15	18	90.0	682	12	BC504723	BC504723 602551929
	16	18	90.0	942	12	BC398850	BC398850 602440491
	17	18	90.0	1024	12	BC330670	BC330670 602560073
	18	17.4	87.0	469	13	BM530983	BM530983 fw99b08.y
c	19	17.4	87.0	613	10	BB635291	BB635291 BB635291
c	20	17.4	87.0	637	14	BO259709	BO259709 faa03b08.
c	21	17.4	87.0	683	10	BE557682	BE557682 fl13a11.y
c	22	17.4	87.0	686	9	AI658162	AI658162 fc19e09.y
	23	17.4	87.0	713	13	B1888410	B1888410 zF637-2.0
	24	17	85.0	410	9	AI249361	AI249361 qx53e12.x
	25	17	85.0	488	14	W38599	W38599 zb19f10.r1
	26	17	85.0	556	17	BM358756	BM358756 CH230-163
	27	17	85.0	562	12	BF666770	BF666770 602121274
	28	17	85.0	639	12	BC668518	BC668518 602310494
	29	17	85.0	647	17	BH304119	BH304119 CH230-4C3
	30	17	85.0	687	12	BC572056	BC572056 602592525
	31	17	85.0	763	13	B1916547	B1916547 603178457
	32	17	85.0	794	17	BH052157	BH052157 RPCI-24-3
	33	16.8	84.0	206	9	AI874007	AI874007 wM47b01.x
c	34	16.8	84.0	212	12	BF094241	BF094241 CM1-UT004
	35	16.8	84.0	267	10	BB092178	BB092178 BB092178
c	36	16.8	84.0	281	9	AI782643	AI782643 EST263522
	37	16.8	84.0	281	14	BM682190	BM682190 UI-E-E01-
c	38	16.8	84.0	282	14	BM729280	BM729280 UI-E-E01-
c	39	16.8	84.0	299	12	BF162756	BF162756 601769216
c	40	16.8	84.0	313	9	AI782644	AI782644 EST263523
	41	16.8	84.0	320	12	BG277660	BG277660 ux47c12.y
	42	16.8	84.0	327	9	AI561366	AI561366 tq48f09.x
c	43	16.8	84.0	336	14	W32334	W32334 zc66a05.r1
c	44	16.8	84.0	361	9	AA172113	AA172113 zP24d03.r
c	45	16.8	84.0	364	12	BC228078	BC228078 ux47c12.x

ALIGNMENTS

RESULT 1
AM176594
LOCUS 150 bp mRNA EST 16-NOV-1999
DEFINITION RC5-CT0070-200899-001.H12 CT0070 Homo sapiens CDNA, mRNA sequence.
ACCESSION AM176594
VERSION AM176594.1 GI:6442631
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 150)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC5ct2-RC5-CT0070-
200899-001-H12ct3-1999-08-20ct4-1)
Seq primer: puc 18 forward
High quality sequence stop: 150.

FEATURES	Location/Qualifiers
SOURCE	1. 150
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_id="CT0070"
	/dev_stage="Adult"
	/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	26 a 55 c 41 g 28 t
ORIGIN	
Query Match	100.0%; Score 20; DB 10; Length 150;
Best Local Similarity	100.0%; Pred. No. 28;
Matches	20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 AGACTGTGAGCTCTTCT 20
Db	42 AGACTGTGAGCTCTTCT 61
RESUL," 2	
AA031826	372 bp mRNA linear EST 09-MAY-1997
LOCUS	zkl4bl1.r1 Soares_pregnant_uterus.NbHPU Homo sapiens cDNA clone
DEFINITION	IMAGE:470493 5' similar to gb:M32315 TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (HUMAN);contains element P7R5 repetitive element ; , mRNA sequence.
ACCESSION	AA031826
VERSION	AA031826.1 GI:1501789
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 372)
AUTHORS	Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissole,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Weg,J., Treaskis,E., Underwood,K., Wohlmann,P., Westleton,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
TITLE	Genome Res. 6 (9), 807-828 (1996)
JOURNAL	97044478
MEDLINE	Contact: Wilson RK
COMMENT	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 849 Std Error: 0.00 Seq primer: -28M3 rev2 from Amersham High quality sequence stop: 362. Location/Qualifiers 1. 372 /organism="Homo sapiens" /db_xref="GDB:3756495" /db_xref="taxon:9606" /clone="IMAGE:470493" /clone_id="Soares_pregnant_uterus_NbHPU" /sex="female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: uterus; Vector: p7773-Pac; Site_1: Not 1; Site_2: Eco RI; 1st strand cDNA was primed with a Not 1 - oligo(dT) primer [5'
FEATURES	
SOURCE	

BASE COUNT	51 a	122 c	102 g	97 t
ORIGIN				
Query Match	100.08;	Score 20;	DB 9;	Length 372;
Best Local Similarity	100.08;	Pred. No. 40;		
Matches 20;	Conservative 100.08;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	AGGACTGTAGGCTCTTCT	20	
Db	39	AGGACTGTAGGCTCTTCT	58	
RESULT 3				
LOCUS	Bi161017	760 bp	mRNA	linear
DEFINITION	602865227.1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:5019247 5' ,			
ACCESSION	mRNA sequence.			
VERSION	Bi161017			
KEYWORDS	Bi161017.1	GI:14621018		
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
JOURNAL	1 (bases 1 to 760)			
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .			
	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapbs-remail.nih.gov			
	Tissue Procurement: ATCC			
	CDNA Library Preparation: Ling Hong/Rubin Laboratory			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LLNL at:			
	http://image.llnl.gov			
	Plate: LTCM1834 row: e column: 08			
	High quality sequence stop: 723.			
FEATURES	Location/Qualifiers			
Source	1..760			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:5019247"			
	/clone_lib="NIH MGC 42"			
	/tissue_type="epitheloid carcinoma cell line"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;			
	Site:2: EcoRI; cDNA made by oligo-dT priming.			
	Directionally cloned into EcoRI/XhoI sites using the			
	following 5' adaptor: GGCACGAG(G). Size-selected >500bp			
	for average insert size 1.8kb. Library constructed by Ling			
	Hong in the laboratory of Gerald M. Rubin (University of			
	California, Berkeley) using ZAP-cDNA synthesis kit			
	(Stratagene) and Superscript II RT (Life Technologies).			
	Note: this is a NIH-MGC Library. 1"			
BASE COUNT	143 a	248 c	245 g	124 t
ORIGIN				
Query Match	100.08;	Score 20;	DB 13;	Length 760;
Best Local Similarity	100.08;	Pred. No. 53;		
Matches 20;	Conservative 100.08;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	AGGACTGTAGGCTCTTCT	20	
Db	592	AGGACTGTAGGCTCTTCT	611	

RESULT 4
BF347834 827 bp mRNA linear EST 22-NOV-2000
LOCUS 602022970F1 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:4158473
DEFINITION 5', mRNA sequence.
ACCESSION BF347834
VERSION BF347834.1 GI:11295429
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 827)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9434 row: k column: 18
High quality sequence stop: 721.
Location/Qualifiers
1..827
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4158473"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (r1 phage-resistant)"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI-CGAP Library."
BASE COUNT 160 a 253 c 273 g 141 t
ORIGIN
Query Match 100.0%; Score 20; DB 12; Length 827;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGACTCTGAGGCTCTTCT 20
|||||
Db 653 AGGACTCTGAGGCTCTTCT 672
RESULT 5
B1160187 845 bp mRNA linear EST 05-JUL-2001
LOCUS 602864057F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:5018007 5',
DEFINITION B1160187
RNA sequence.
ACCESSION B1160187
VERSION B1160187.1 GI:14620188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 845)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1831 row: a column: 16
High quality sequence stop: 845.
Location/Qualifiers
1..845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5018007"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOT87; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAGC. Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library. |"
BASE COUNT 147 a 258 c 261 g 179 t
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Query Match 100.0%; Score 20; DB 13; Length 845;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGGACTCTGAGGCTCTTCT 20
|||||
Db 633 AGGACTCTGAGGCTCTTCT 652
RESULT 6
BG829828 932 bp mRNA linear EST 22-MAY-2001
LOCUS 602764119F1 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:4899436 5',
DEFINITION BG829828
RNA sequence.
ACCESSION BG829828
VERSION BG829828.1 GI:14177415
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 932)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM1791 row: e column: 05
High quality sequence stop: 833.
Location/Qualifiers
1..932
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4899436"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOT87; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library. 1"

BASE COUNT 162 a 296 c 296 g 177 t 1 others

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 932;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTGTGAGCTCTTTCT 20
|||||

Db 593 AGGACTGTGAGCTCTTTCT 612

RESULT 7
BF568409 1051 bp mRNA linear EST 12-DEC-2000
LOCUS 60218440BF1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300633 5',
DEFINITION mRNA sequence.
ACCESSION BF568409
VERSION BF568409.1 GI:11641789
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1051)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov
Plate: L16M1159 row: c column: 02
High quality sequence stop: 769.
Location/Qualifiers

FEATURES
Source 1..1051
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4300633"
/clone_lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library. 1"

BASE COUNT 229 a 313 c 346 g 161 t 2 others

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 1051;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTGTGAGCTCTTTCT 20
|||||

Db 592 AGGACTGTGAGCTCTTTCT 611

RESULT 8
BQ052282 1053 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT 6868457 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935311
DEFINITION 5', mRNA sequence.
ACCESSION BQ052282
VERSION BQ052282.1 GI:19811622
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1053)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov
Plate: L16M2118 row: c column: 16
High quality sequence stop: 649.
Location/Qualifiers

FEATURES
Source 1..1053
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5935311"
/clone_lib="NIH_MGC_106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library. 1"

BASE COUNT 216 a 328 c 297 g 212 t

ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 1053;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTGTGAGCTCTTTCT 20
|||||

Db 826 AGGACTGTGAGCTCTTTCT 807

RESULT 9
BF568708 1066 bp mRNA linear EST 12-DEC-2000
LOCUS 602184353F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300500 5',
DEFINITION mRNA sequence.
ACCESSION BF568708
VERSION BF568708.1 GI:11642088
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1066)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LNCM1159 row: 1 column: 13
High quality sequence stop: 712.

FEATURES
source 1..1066
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4300500"
/clone_1lb="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. 1"

BASE COUNT 216 a 316 c 354 g 180 t
ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 1066;
Best Local Similarity 100.0%; Pred. NO. 60;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGACTCTGAGCCTCTTCT 20
|||||
Db 477 AGGACTCTGAGCCTCTTCT 496

RESULT 10 1102 bp mRNA linear EST 12-MAR-2002
BM917316
LOCUS
DEFINITION AGNCOURT_6606593 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483819
5', mRNA sequence.
ACCESSION BM917316
VERSION BM917316
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1102)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/MCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LNCM2012 row: b column: 12
High quality sequence stop: 507.
Location/Qualifiers

FEATURES
source 1..1102
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5483819"
/clone_1lb="NIH_MGC_106"

/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 219 a 366 c 292 g 222 t 3 others
ORIGIN

Query Match 100.0%; Score 20; DB 14; Length 1102;
Best Local Similarity 100.0%; Pred. NO. 61;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AGGACTCTGAGCCTCTTCT 20
|||||
Db 93 AGGACTCTGAGCCTCTTCT 112

RESULT 11 2291 bp mRNA linear HTC 02-AUG-2001
BC011844
LOCUS
DEFINITION Homo sapiens, similar to tumor necrosis factor receptor superfamily, member 1B, clone IMAGE:4111730, mRNA.
BC011844
VERSION BC011844.1 GI:15080140
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2291)
Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc-mgc@nhgri.nih.gov
Shewchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-U., Karlins, E., Legaspi, R., Lim, M., Maduro, Q., Mastello, C., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantrilop, S., Thomas, P. J., Tomson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Series: IRAL Plate: 28 Row: 1 Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: incomplete processing.
Location/Qualifiers

FEATURES
source 1..2291
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4111730"
/tissue_type="muscle, rhabdomyosarcoma"

clone_lib="NIH_MGC_17"
lab_host="DH10B-R"
/note="Vector: pOTB7"

BASE COUNT 461 a 708 c 713 g 409 t

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 2291;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGCCTCTTCT 20
|||||

Db 1480 AGGACTCTGAGCCTCTTCT 1499

RESULT 12
AM062603 175 bp mRNA linear EST 06-OCT-1999
DEFINITION RC0-CT0088-050899-001-B07 CT0088 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM062603
VERSION AM062603.1 GI:6013988
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 175)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC0-CT0088-050899-001-B07&f3=1999-08-05&f4=1>)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 175.
Location/Qualifiers
1..175
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0088"
/dev_stage="Adult"
/note="Organ: Colon; Vector: pUC18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 32 a 65 c 46 g 32 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 175;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGCCTCTTCT 20
|||||

Db 66 AGGACTCTGAGCCTCTTCT 85

RESULT 13
AG129979/c 602 bp DNA linear GSS 04-NOV-2001
LOCUS

DEFINITION Pan troglodytes DNA, clone: PTB-14J18.F, genomic survey sequence.
ACCESSION AG129979
VERSION AG129979.1 GI:16659144
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC library clone:PTB-14J18.F.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
2 (bases 1 to 602)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
DIRECT SUBMISSION
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpses@sc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB this BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..602
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-14J18.F"
/sex="male"
/cell_type="Lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 154 a 143 c 101 g 204 t

ORIGIN

Query Match 92.0%; Score 18.4; DB 17; Length 602;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AGGACTCTGAGCCTCTTCT 20
|||||

Db 465 AGGACTCTGAGCCTCTTGT 446

RESULT 14
AZ803826 562 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0064J19F Mouse 10kb plasmid UUCIM library Mus musculus genomic
DEFINITION clone UUCG2M0064J19 F, DNA sequence.
ACCESSION AZ803826
VERSION AZ803826.1 GI:12956149
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 562)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0064 row: J column: 19
Seq primer: CGTTGTAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 562.
Location/Qualifiers

FEATURES
source

1. 562
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0064J19"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g11473211419b1AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 191 a 104 c 116 g 151 t
ORIGIN

Query Match 90.0%; Score 18; DB 17; Length 562;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACTCTGAGGCTCTTCT 20
|||||
Db 395 GACTCTGAGGCTCTTCT 378

RESULT 15
BG504723 682 bp mRNA linear EST 27-MAR-2001
LOCUS 602551929P1 NIH_MGC_61 Homo sapiens CDNA IMAGE:4664527 5',
DEFINITION mRNA sequence.
ACCESSION BG504723
VERSION BG504723.1 GI:13466240
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.C.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.C.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1468 row: 1 column: 08
High quality sequence stop: 628.
Location/Qualifiers

FEATURES
source

1. 682
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4664527"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: S111 (ggccgctcgcc); Site_2: S111 (ggccatattggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dT(30)BR-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT 226 a 141 c 164 g 151 t
ORIGIN

Query Match 90.0%; Score 18; DB 12; Length 682;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACTCTGAGGCTCTTTC 19
|||||
Db 1 GGACTCTGAGGCTCTTTC 18

Search completed: December 6, 2002, 04:54:31
Job time : 50.2783 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:41:08 : Search time 1.03896 Seconds
(without alignments)
5903.528 Million cell updates/sec

Title: US-09-856-937A-4

Sequence: 1 aggactctgagcctcttct 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCNUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	1641 1 US-08-385-229-1	Sequence 1, Appl 1
2	20	100.0	1641 2 US-08-650-000-1	Sequence 1, Appl 1
3	20	100.0	1641 6 5395760-1	Patent No. 5395760
4	20	100.0	2224 4 US-08-477-347-2	Sequence 2, Appl 1
5	20	100.0	2224 4 US-08-476-862-1	Sequence 1, Appl 1
6	20	100.0	3683 4 US-09-844-634-3	Sequence 3, Appl 1
7	20	100.0	15602 4 US-09-844-634-17	Sequence 17, Appl 1
8	16	80.0	1318 5 PCT-US94-07127A-1	Sequence 1, Appl 1
9	16	80.0	1336 4 US-09-257-179-13	Sequence 13, Appl 1
10	15.8	79.0	2064 3 US-08-875-944B-1	Sequence 1, Appl 1
11	15.8	79.0	2064 4 US-09-116-049-3	Sequence 3, Appl 1
12	15.8	79.0	98844 4 US-09-791-211-10	Sequence 10, Appl 1
13	15.2	76.0	321 2 US-08-232-081B-35	Sequence 35, Appl 1
14	15.2	76.0	321 2 US-08-232-081B-35	Sequence 35, Appl 1
15	15.2	76.0	678 4 US-09-605-785-605	Sequence 605, App
16	15.2	76.0	678 4 US-09-605-785-664	Sequence 604, App
17	15.2	76.0	694 4 US-09-605-785-604	Sequence 604, App
18	15.2	76.0	694 4 US-09-605-785-665	Sequence 665, App
19	15.2	76.0	705 4 US-09-605-785-666	Sequence 666, App
20	15.2	76.0	817 4 US-09-605-785-603	Sequence 603, App
21	15.2	76.0	817 4 US-09-605-785-667	Sequence 667, App
22	15.2	76.0	854 4 US-09-247-155-67	Sequence 67, App 1
23	15.2	76.0	1488 2 US-08-687-559-5	Sequence 5, Appl 1
24	15.2	76.0	1805 4 US-08-961-527-247	Sequence 247, App
25	15.2	76.0	5599 2 US-08-477-451-9	Sequence 9, Appl 1
26	15.2	76.0	5599 2 US-08-477-451-13	Sequence 13, Appl 1
27	15.2	76.0	9495 1 US-08-271-829-1	Sequence 1, Appl 1

C 28	15.2	76.0	9495 5 PCT-US93-01544-1	Sequence 1, Appl 1
C 29	15.2	76.0	19932 2 US-08-477-451-25	Sequence 25, Appl 1
C 30	14.8	74.0	639 1 US-08-480-784-26	Sequence 26, Appl 1
C 31	14.8	74.0	639 1 US-08-483-553-26	Sequence 26, Appl 1
C 32	14.8	74.0	639 1 US-08-487-002-26	Sequence 26, Appl 1
C 33	14.8	74.0	639 1 US-08-483-554B-26	Sequence 26, Appl 1
C 34	14.8	74.0	639 1 US-08-488-011B-26	Sequence 26, Appl 1
C 35	14.8	74.0	639 4 US-08-488-011B-26	Sequence 26, Appl 1
C 36	14.8	74.0	639 5 PCT-US95-10202-26	Sequence 26, Appl 1
C 37	14.8	74.0	639 5 PCT-US95-10203-26	Sequence 26, Appl 1
C 38	14.8	74.0	639 5 PCT-US95-10220-26	Sequence 26, Appl 1
C 39	14.8	74.0	646 4 US-09-222-575-79	Sequence 29, Appl 1
C 40	14.8	74.0	2492 3 US-08-695-191-3	Sequence 3, Appl 1
C 41	14.8	74.0	2492 3 US-08-682-080-3	Sequence 3, Appl 1
C 42	14.8	74.0	3227 4 US-09-221-017B-451	Sequence 451, App
C 43	14.8	74.0	4041 1 US-08-147-812-4	Sequence 4, Appl 1
C 44	14.8	74.0	4110 3 US-09-123-708-1	Sequence 1, Appl 1
C 45	14.8	74.0	4110 3 US-09-123-624-1	Sequence 1, Appl 1

ALIGNMENTS

RESULT 1
: Sequence 1, Application US/08385229
: Patent No: 5605690

GENERAL INFORMATION:

: APPLICANT: Jacobs, Cindy A.

: TITLE OF INVENTION: Method of Treating TNF-Dependent

: TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists

: NUMBER OF SEQUENCES: 5

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Immunex Corporation

: STREET: 51 University Street

: CITY: Seattle

: STATE: Washington

: COUNTRY: U.S.A.

: ZIP: 98101

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/385,229

: FILING DATE:

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US/07/946,236

: FILING DATE:

: ATTORNEY/AGENT INFORMATION:

: NAME: Wright, Christopher L.

: REGISTRATION NUMBER: 31,680

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (206) 587-0430

: TELEFAX: (206) 587-0606

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 1641 base pairs

: TYPE: nucleic acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: MOLECULE TYPE: cDNA

: HYPOTHETICAL: NO

: ANTI-SENSE: NO

: ORIGINAL SOURCE:

: ORGANISM: Homo sapiens

: CELL TYPE: Fibroblast

: CELL LINE: WI-26 V44

: IMMEDIATE SOURCE:

LIBRARY: WI-26 VA4
CLONE: Clone 1
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1473
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 154..1470
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 88..153
US-08-385-229-1

Query Match 100.0%; Score 20; DB 1; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGGCTCTTCT 20
Db 1569 AGGACTGTGAGGCTCTTCT 1588

RESULT 2
US-08-650-000-1
Sequence 1, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1641 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Fibroblast
CELL LINE: WI-26 VA4
IMMEDIATE SOURCE:
LIBRARY: WI-26 VA4
CLONE: 1
FEATURE:
NAME/KEY: CDS
LOCATION: 88..1473
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 154..1470
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 88..153
PUBLICATION INFORMATION:
AUTHORS: Smith, Craig A.
AUTHORS: Davis, Terri
AUTHORS: Anderson, Dirk
AUTHORS: Solam, Lisabeth
AUTHORS: Beckmann, M. P.
AUTHORS: Jerzy, Rita
AUTHORS: Dower, Steven K.
AUTHORS: Cosman, David
AUTHORS: Goodwin, Raymond G.
TITLE: A Receptor for Tumor Necrosis Factor Defines
TITLE: an Unusual Family of Cellular and Viral Proteins
JOURNAL: Science
VOLUME: 248
PAGES: 1019-1023
DATE: 25-MAY-1990
US-08-650-000-1

Query Match 100.0%; Score 20; DB 2; Length 1641;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGGCTCTTCT 20
Db 1569 AGGACTGTGAGGCTCTTCT 1588

RESULT 3
5395760-1
Patent No. 5395760
APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN, M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR- α AND β -RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ. ID NO: 1:
LENGTH: 1641
5395760-1

Query Match 100.0%; Score 20; DB 6; Length 1641;

Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGACTCTGAGCTCTTTCT 20
|||||
Db 1569 AGACTCTGAGCTCTTTCT 1588

RESULT 4
US-08-477-347-2
Sequence 2, Application US/08477347
Patent No. 6232446
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,665
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472
US-08-477-347-2
Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGACTCTGAGCTCTTTCT 20
|||||
Db 1571 AGACTCTGAGCTCTTTCT 1590
RESULT 5
US-08-476-862-1
Sequence 1, Application US/08476862

Patent No. 6262239
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 90..1472
US-08-476-862-1
Query Match 100.0%; Score 20; DB 4; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AGACTCTGAGCTCTTTCT 20
|||||
Db 1571 AGACTCTGAGCTCTTTCT 1590
RESULT 6
US-09-844-634-3
Sequence 3, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRE

```
FILE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 3
LENGTH: 3683
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (90)...(1475)
US-09-844-634-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 3683;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTGTGAGGCTCTTCT 20
DB 1571 AGACTGTGAGGCTCTTCT 1590

RESULT 7
US-09-844-634-17
Sequence 17, Application US/09844634
Patent No. 6410324
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
FILE OF INVENTION: ANTISENSE MODULATION OF TUMOR NECROSIS FACTOR RECEPTOR 2 EXPRESSION
TITLE REFERENCE: RTS-0216
CURRENT APPLICATION NUMBER: US/09/844,634
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 17
LENGTH: 15602
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-844-634-17

Query Match
Best Local Similarity 100.0%; Score 20; DB 4; Length 15602;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGACTGTGAGGCTCTTCT 20
DB 11104 AGACTGTGAGGCTCTTCT 11123

RESULT 8
PCT-US94-07127A-1
Sequence 1, Application PC/TUS9407127A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Interleukin-1 Converting Enzyme Like Apoptosis Protease-1, an
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESS: CECCH, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07127A
FILING DATE: submitted herewith
```

```
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-184
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1318 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US94-07127A-1

Query Match
Best Local Similarity 80.0%; Score 16; DB 5; Length 1318;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ACTCTGAGGCTCTTC 19
DB 12 ACTCTGAGGCTCTTC 27

RESULT 9
US-09-257-179-13/C
Sequence 13, Application US/09257179
Patent No. 6410709
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/257,179
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US98/17709
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 60/056,270
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,247
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,073
EARLIER FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 1336
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (766)
OTHER INFORMATION: n equals a,t,g, or c
US-09-257-179-13

Query Match
Best Local Similarity 80.0%; Score 16; DB 4; Length 1336;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AGACTGTGAGGCTCTTCT 20
DB 232 AGGATTTGAGGCTGTCT 213

RESULT 10
US-08-875-944B-1/C
Sequence 1, Application US/08875944B
```

Patent No. 6096542
GENERAL INFORMATION:
APPLICANT: FUJINAGA, Kei
APPLICANT: YOSHIDA, Koichi
APPLICANT: HIGASHINO, Fumihito
TITLE OF INVENTION: CANCER CONTROL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,944B
FILING DATE: 07-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 07-020173
FILING DATE: 08-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00016
FILING DATE: 09-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: FUJINAGA-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1386
US-08-875-944B-1

Query Match 79.0%; Score 15.8; DB 3; Length 2064;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACTGTGAGCTCTTCT 20
DB 239 GGACTGTGAGCTCTTCT 221

RESULT 11
US-09-116-049-3/C
Sequence 3, Application US/09116049A
Patent No. 6248351
GENERAL INFORMATION:
APPLICANT: Hung, Men-Chie
TITLE OF INVENTION: HUMAN PEAK IS A TUMOR SUPPRESSOR FOR CANCER CELLS
FILE REFERENCE: UTS:582
CURRENT APPLICATION NUMBER: US/09/116,049A
CURRENT FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2064
TYPE: DNA
ORGANISM: Homo sapiens

US-09-116-049-3
Query Match 79.0%; Score 15.8; DB 4; Length 2064;
Best Local Similarity 89.5%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGACTGTGAGCTCTTCT 20
DB 239 GGACTGTGAGCTCTTCT 221

RESULT 12
US-09-791-211-10
Sequence 10, Application US/09791211
Patent No. 6448080
GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 98844
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 24962
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 64383
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65468
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65469
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 87130
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 89049
OTHER INFORMATION: unknown
OTHER INFORMATION: unknown
US-09-791-211-10

Query Match 79.0%; Score 15.8; DB 4; Length 98844;
Best Local Similarity 89.5%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGGACTGTGAGCTCTTCT 19
DB 41628 AGGCACTGTGAGCTCTTCT 41646

RESULT 13
US-08-232-081B-35/C
Sequence 35, Application US/08232081B
Patent No. 5886152
GENERAL INFORMATION:
APPLICANT: NAKATANI, TOMOYUKI
APPLICANT: GOMI, HIDEYUKI
APPLICANT: WIDENES, JOHN
APPLICANT: NOGUCHI, HINOSHI

```
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-232-081B-35

Query Match          76.0%  Score 15.2;  DB 2;  Length 321;
Best Local Similarity 85.0%  Pred. No. 71;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1 AGGACTCTGAGGCTCTTCT 20
        |||||  || |||||
Db      67 AGGACAGTGTGCTCTTCT 48

RESULT 14
US-08-232-081B-36/C
; Sequence 36, Application US/08232081B
; Patent No. 5886152
; GENERAL INFORMATION:
; APPLICANT: NAKATANI, TOMOYUKI
; APPLICANT: GOMI, HIDEYUKI
; APPLICANT: WIDENES, JOHN
; APPLICANT: NOGUCHI, HIROSHI
; TITLE OF INVENTION: HUMANIZED B-B10
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,081B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SVENSSON, LEONARD R
; REGISTRATION NUMBER: 30,330
```

```
; REFERENCE/DOCKET NUMBER: 20-3484
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-232-081B-36

Query Match          76.0%  Score 15.2;  DB 2;  Length 321;
Best Local Similarity 85.0%  Pred. No. 71;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1 AGGACTCTGAGGCTCTTCT 20
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Db      67 AGGACAGTGTGCTCTTCT 48

RESULT 15
US-09-605-785-605
; Sequence 605, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121 427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 605
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(678)
; OTHER INFORMATION: n = A,T,C or G
; US-09-605-785-605

Query Match          76.0%  Score 15.2;  DB 4;  Length 678;
Best Local Similarity 85.0%  Pred. No. 77;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      1 AGGACTCTGAGGCTCTTCT 20
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Db      432 AGGACTCTGTGCTCTTCT 451

Search completed: December 5, 2002, 23:39:10
Job time : 34.039 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 20:03:23 Search time 0.972171 Seconds

(without alignments)
8021.899 Million cell updates/sec

Title: US-09-856-937a-4

Sequence: 1 aggaactctgagcctcttct 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 350425 segs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	1641	10 US-09-758-124-1	Sequence 1, Appl1
2	20	100.0	2224	10 US-09-800-909-1	Sequence 1, Appl1
3	20	100.0	2224	10 US-09-800-908-2	Sequence 2, Appl1
4	20	100.0	3683	10 US-09-954-456-1187	Sequence 1187, Ap
5	16.8	84.0	480	10 US-09-864-761-423	Sequence 423, App
6	16.8	84.0	580	10 US-09-867-701-6135	Sequence 6135, Ap
7	16.8	84.0	966	10 US-09-864-761-17222	Sequence 17222, A
8	16.8	84.0	1086	10 US-09-864-761-17120	Sequence 17120, A
9	16.8	84.0	1086	10 US-09-864-761-17617	Sequence 17617, A
10	16	80.0	526	10 US-09-864-761-12705	Sequence 12705, A
11	16	80.0	1336	10 US-09-729-835-113	Sequence 13, Appl1
12	15.8	79.0	239	9 US-10-002-344A-72	Sequence 72, Appl1
13	15.8	79.0	333	9 US-10-002-344A-73	Sequence 73, Appl1
14	15.8	79.0	527	10 US-09-867-550-1063	Sequence 1063, Ap
15	15.8	79.0	527	10 US-09-867-550-2118	Sequence 2118, Ap
16	15.8	79.0	2333	10 US-09-920-300A-1788	Sequence 1788, Ap
17	15.8	79.0	2333	10 US-09-880-107-3316	Sequence 3316, Ap
18	15.8	79.0	2333	12 US-10-033-528-1788	Sequence 1788, Ap
19	15.4	77.0	433	10 US-09-867-701-10530	Sequence 10530, A

20	15.4	77.0	582	10 US-09-864-761-9755	Sequence 9755, Ap
21	15.2	76.0	248	10 US-09-983-965-3631	Sequence 3631, Ap
22	15.2	76.0	275	10 US-09-783-590-728	Sequence 728, App
23	15.2	76.0	300	10 US-09-815-242-9225	Sequence 9225, Ap
24	15.2	76.0	300	10 US-09-815-242-9436	Sequence 9436, Ap
25	15.2	76.0	313	10 US-09-983-965-909	Sequence 909, App
26	15.2	76.0	438	10 US-09-960-352-12682	Sequence 12682, A
27	15.2	76.0	515	10 US-09-777-564-81	Sequence 81, Appl1
28	15.2	76.0	549	10 US-09-864-761-7389	Sequence 7389, Ap
29	15.2	76.0	590	10 US-09-777-564-543	Sequence 543, App
30	15.2	76.0	615	10 US-09-777-564-25	Sequence 25, Appl1
31	15.2	76.0	678	10 US-09-759-143-605	Sequence 605, App
32	15.2	76.0	678	10 US-09-759-143-664	Sequence 664, App
33	15.2	76.0	678	10 US-09-780-669-605	Sequence 605, App
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36	15.2	76.0	678	10 US-09-822-827-664	Sequence 664, App
37	15.2	76.0	694	10 US-09-759-143-604	Sequence 604, App
38	15.2	76.0	694	10 US-09-759-143-665	Sequence 665, App
39	15.2	76.0	694	10 US-09-780-669-604	Sequence 604, App
40	15.2	76.0	694	10 US-09-780-669-665	Sequence 665, App
41	15.2	76.0	694	10 US-09-822-827-604	Sequence 604, App
42	15.2	76.0	694	10 US-09-822-827-665	Sequence 665, App
43	15.2	76.0	705	10 US-09-759-143-666	Sequence 666, App
44	15.2	76.0	705	10 US-09-780-669-666	Sequence 666, App
45	15.2	76.0	705	10 US-09-822-827-666	Sequence 666, App

ALIGNMENTS

RESULT 1
US-09-758-124-1
Sequence 1, Application US/09758124
Patent No. US20020006391A1
GENERAL INFORMATION:
APPLICANT: SMITH, Craig A.
APPLICANT: GOODMAN, Raymond G.
APPLICANT: BECKMANN, M. Patricia
TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
FILE REFERENCE: A7895
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 08/953,268
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 08/555,629
PRIOR FILING DATE: 1995-11-09
PRIOR APPLICATION NUMBER: 08/468,453
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/038,765
PRIOR FILING DATE: 1993-03-13
PRIOR APPLICATION NUMBER: 07/523,635
PRIOR FILING DATE: 1990-05-10
PRIOR APPLICATION NUMBER: 07/421,417
PRIOR FILING DATE: 1989-10-13
PRIOR APPLICATION NUMBER: 07/405,370
PRIOR FILING DATE: 1989-09-11
PRIOR APPLICATION NUMBER: 07/403,241
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1641
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (88)..(1473)
NAME/KEY: mat_peptide
LOCATION: (154)..(1470)
NAME/KEY: sig_peptide
LOCATION: (88)..(153)
US-09-758-124-1

Db	2667	CCACACATCTCCCTTTCAGGGAATTTCAGAGACTAAGATGACTAGTCTCTGACCAT	2722
Qy	1657	CTCTACTCTCTACCTCAGCCTAGACCTCTCCCTCCAGAGGGGTGGTTCCTTC	1716
Db	2727	CTCTCTACTCTCTACCTCAGCCTAGACCTCTCCCTCCAGAGGGGTGGTTCCTTC	2788
Qy	1717	CCCACTCCCCCACTTCAATTCTGGGGCCCCAAACGGGCTGCCCTGCCACTTTGGTACATG	1777
Db	2787	CCCACTCCCCCACTTCAATTCTGGGGCCCCAAACGGGCTGCCCTGCCACTTTGGTACATG	2844
Qy	1777	GCGAGTGAATCCCAAGTGGCAGCTTGTCGCGTCGTCGTGTGGTGGTCGCGGGGTGG	1833
Db	2847	GCGAGTGAATCCCAAGTGGCAGCTTGTCGCGTCGTCGTGTGGTGGTCGCGGGGTGG	2900
Qy	1837	TGTAGCAAGGTCGGTAAGTTGATGAGCTGCCCTTGATGAAGCACTGAAGCTGGGATTCTTC	1894
Db	2907	TGTAGCAAGGTCGGTAAGTTGATGAGCTGCCCTTGATGAAGCACTGAAGCTGGGATTCTTC	2966
Qy	1887	CCCATTTAGATGACGCTTCCCCCTCCAGGGCCAGGGCCCTGCAGAGGGGAAACCATGTG	1955
Db	2967	CCCATTTAGATGACGCTTCCCCCTCCAGGGCCAGGGCCCTGCAGAGGGGAAACCATGTG	3022
Qy	1957	AGCCTTGCCCGGATTCCTGGGGGGAAGAGGTTGAGGGGGCTCGGAAGGCTCAGTCTCA	2011
Db	3027	AGCCTTGCCCGGATTCCTGGGGGGAAGAGGTTGAGGGGGCTCGGAAGGCTCAGTCTCA	3088
Qy	2017	GGAGCATGGGGATTAAGGAGAAAGCATGAATTTGTCTACGACGACAGGGCCAGGGTGATA	2077
Db	3087	GGAGCATGGGGATTAAGGAGAAAGCATGAATTTGTCTACGACGACAGGGCCAGGGTGATA	3144
Qy	2077	AATTGTGATTAATTTCCACTGAGCTTGAGCTTGGCAGCTGACTGACTATTGGAGGGTGGAGA	2133
Db	3147	AATTGTGATTAATTTCCACTGAGCTTGAGCTTGGCAGCTGACTGACTATTGGAGGGTGGAGA	3200
Qy	2137	GCCCAAGCATTAACATGGAGACAAGAGGGTTTTCCACCCTGGAAATCAGATGTCAGACT	2199
Db	3207	GCCCAAGCATTAACATGGAGACAAGAGGGTTTTCCACCCTGGAAATCAGATGTCAGACT	3266
Qy	2197	GACCTGGCTGACAGTACGACGACCTGTACTCAGAGAGGCTGAGGGGAGGATCACTGGAGCCC	2255
Db	3267	GACCTGGCTGACAGTACGACGACCTGTACTCAGAGAGGCTGAGGGGAGGATCACTGGAGCCC	3332
Qy	2257	AGGAGTTTGAGGCTGCAGACGACATGATGCGCGCACTACACTCACAACCTGAGCAACAGA	2311
Db	3327	AGGAGTTTGAGGCTGCAGACGACATGATGCGCGCACTACACTCACAACCTGAGCAACAGA	3388
Qy	2317	GTGAGACCCCTGTCTTTAAGAAAAAAAAGTCAGACTGCTGGGACTGGCCAGGTTTCTG	2377
Db	3387	GTGAGACCCCTGTCTTTAAGAAAAAAAAGTCAGACTGCTGGGACTGGCCAGGTTTCTG	3444
Qy	2377	CCCAATTGGACCCACATGAGAGATGATGATGAGGAGGCACTGGCCCCCTGGGAGAGGCT	2433
Db	3447	CCCAATTGGACCCACATGAGAGATGATGATGAGGAGGCACTGGCCCCCTGGGAGAGGCT	3500
Qy	2437	GGGAGAACCTTAGGCTTCTTGGCATCACAGGGCAGACCGGGGAAGCGATGAATTTGGAG	2499
Db	3507	GGGAGAACCTTAGGCTTCTTGGCATCACAGGGCAGACCGGGGAAGCGATGAATTTGGAG	3566
Qy	2497	ACTCTGTGGGGCTTGGTTCCCTTGTGTGTGTGTGTGTGTGATCCCAAGACAAATGAAGTTTG	2555
Db	3567	ACTCTGTGGGGCTTGGTTCCCTTGTGTGTGTGTGTGTGTGATCCCAAGACAAATGAAGTTTG	3622
Qy	2557	CACCTATAGCTGAGAGCGCATTCCTGCTATCAATAAACCCTGTTTGTAAAAAAA 2613	
Db	3627	CACCTATAGCTGAGAGCGCATTCCTGCTATCAATAAACCCTGTTTGTAAAAAAA 3683	
RESULT 7			
AAO10956			
ID AAO10956 standard; DNA; 2339 BP.			
xx			
AC AAO10956;			

XX 24-MAY-1991 (first entry)
 DT Encodes human 75kd TNF-binding protein.
 DE
 XX Tumour Necrosis Factor; binding proteins; septic shock;
 KM autoimmune glomerulonephritis; lymphokine; cytokine..
 KW
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1179
 FT /tag= a
 FT /product= 75kd TNF-BP
 FT
 EP417563-A.
 XX
 PD 20-MAR-1991.
 XX
 XX 31-AUG-1990; 90EP-0116707.
 XX
 XX 20-APR-1990; 90CH-0001347.
 PR 12-SEP-1989; 89CH-0003319.
 PR 08-MAR-1990; 90CH-0000746.
 XX
 XX (HOFF) HOFFMANN-LA ROCHE AG.
 PA
 XX BrocKhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;
 PI Schlaeger EJ;
 PI
 DR WPI: 1991-081851/12.
 DR P-PSDB; AAR11605.
 PS
 XX
 PS Claim 4; Fig 1: 26pp; German.
 CC Partial amino acid sequences were determined for the 55 and 75kd
 CC TNF-BPs (see ARI1072-R11081) and oligonucleotide primers were
 CC synthesised based on these partial sequences. The primers were used
 CC to produce a cDNA fragment for use as a probe to screen a human
 CC placental cDNA bank constructed in lambda gtl1. Positive clones were
 CC identified and sequenced. Repeated sequencing showed a discrepancy
 CC at position 7 such that the third codon encodes either Thr or Ser.
 CC DNA constructs comprising the TNF-BP coding sequence may also
 CC contain a fragment encoding a human Ig domain. Recombinant
 CC constructs are used to transform cells to confer improved TNF-
 CC binding properties.
 CC See also AAO10955.
 CC
 SQ Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other;
 Query Match 54.5%; Score 1423; DB 12; Length 2339;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 1457; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

Db 1103 CAGAGACCTGTGGGAGACCCGAGAGAGAGCCCTGCCCCCTGGATGCTGATGCTG 1162
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 QY 389 GATGAAGCCCACTTAACAGAGCCGGTGTGGGCTGTGTGTAGCCAAAGTGGGCTAGACC 448
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 Db 1163 GGATGAAGCCCACTTAACAGAGCCGGTGTGGGCTGTGTGTAGCCAAAGT -GGTGAAGCC 1221
 |||||||
 QY 449 CTGGCAGATGACCTTCGCAAGAGGGCCCTGTCTTCACAGGCCCCACACATAGACTCT 508
 |||||||
 Db 1222 CTGGCAGATGACCTTCGCAAGAGGGCCCTGTCTTCACAGGCCCCACACATAGACTCT 1281
 |||||||
 QY 509 GAGCCTCTTCGCGCAAGTCTCTAGTGGCCCTCAGAGCCGAGCCCTCCCTGTGACC 568
 |||||||
 Db 1282 GAGCCTCTTCGCGCAAGTCTCTAGTGGCCCTCAGAGCCGAGCCCTCCCTGTGACC 1341
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 QY 569 TCGAGCCCAAGACAGAGGAGGAGAGTGTGGGAAACCTCTGTGCAATGTGTGTCCCT 628
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 Db 1342 TCGAGCCCAAGACAGAGGAGGAGAGTGTGGGAAACCTCTGTGCAATGTGTGTCCCT 1401
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 QY 629 CTGGAAAGCTGGCTGGGCAATGACGTTCCGGGCATGTGTGGGCAAGTCCCTGACTCTCT 688
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 Db 1402 CTGGAAAGCTGGCTGGGCAATGACGTTCCGGGCATGTGTGGGCAAGTCCCTGACTCTCT 1461
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 QY 689 GTGACCTGCCCCGCCAGCTGCACTGCGACCTGCGGCTTGAGAGCCCTTGAGGCTTTTGG 748
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 QY 749 TTTGTTTGTGTTTGTGTTTGTGTTTCTCCCCCTGGGCTCTGCCAGCTGTGGCTTCCA 808
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 QY 809 GAAACCCCAAGCATCTTTTCTGCAAGAGGGGCTTCTGAGAGAGAGAGGAGTGGCTGTAG 868
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 Db 1582 GAAACCCCAAGCATCTTTTCTGCAAGAGGGGCTTCTGAGAGAGAGAGGAGTGGCTGTAG 1641
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 QY 869 TCACCATGAAGACAGACAGTGTCTCAGCCTGAGCCTGAGACTGCGGATGTGCTCTGGG 928
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 Db 1642 TCACCATGAAGACAGACAGTGTCTCAGCCTGAGCCTGAGACTGCGGATGTGCTCTGGG 1701
 |||||||
 QY 929 GCTGTGTAGGAGAGAGTGTGGCAGCCCTGTAGGAAACGGGCTCTTCAAGTTAGCTCAG 988
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 Db 1702 GCTGTGTAGGAGAGAGTGTGGCAGCCCTGTAGGAAACGGGCTCTTCAAGTTAGCTCAG 1761
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 QY 989 GAGGCTTGAAAGCATCCTCCTCAGAGGCCAGGTGCAAGCTCATGATCCAGACAG 1048
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 Db 1762 GAGGCTTGAAAGCATCCTCCTCAGAGGCCAGGTGCAAGCTCATGATCCAGACAG 1821
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 QY 1049 TTTGGAGAGCTGAGGCGGGTGGATCAGCTGAGGTTAGAGATTTCAGACAGACCTGGCCAA 1108
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 Db 1822 TTTGGAGAGCTGAGGCGGGTGGATCAGCTGAGGTTAGAGATTTCAGACAGACCTGGCCAA 1881
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 QY 1109 CATGCTAAACCCCATCTCTCTAATAAATACAGAAATTAAGCCGGGCTGTGGGGGAC 1168
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 Db 1882 CATGCTAAACCCCATCTCTCTAATAAATACAGAAATTAAGCCGGGCTGTGGGGGAC 1941
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 QY 1169 CATATGCTCCAGCTCTCAGAGAGCCCTGAGGAAATCTTTGAACCCGGGAAGGGA 1228
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 Db 1942 CATATGCTCCAGCTCTCAGAGAGCCCTGAGGAAATCTTTGAACCCGGGAAGGGA 2001
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 QY 1229 GGTTCCAGGAGCCGAGATCAAGCCACTGCACTCCAGCTGGGGGAGACAGAGCAGAGTCT 1288
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 Db 2002 GGTTCCAGGAGCCGAGATCAAGCCACTGCACTCCAGCTGGGGGAGACAGAGCAGAGTCT 2061
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 QY 1289 GTCTCAAAAGAAAAAAGCAAGCCCTCTCAAAATCTTAATCTTGTCTTTTATACAT 1348
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 Db 2062 GTCTCAAAAG -AAAAAAGCAAGCCCTCTCAAAATCTTAATCTTGTCTTTTATACAT 2120
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 QY 1349 GGTGTGAAGTACAGATGCCAGAGAGGCCAGAGAGCCACCATATTCAGTCTGTGGCT 1408
 |||||||
 Db 2121 GGTGTGAAGTACAGATGCCAGAGAGGCCAGAGAGCCACCATATTCAGTCTGTGGCT 2180
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 QY 1409 GGGCAAGATACGCACTTCAATCAAGAAATCTGCCAATTTTTTAAAAAAGTAACTACAC 1468
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Best Local Similarity 98.58; Pred. No. 0;

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CCCCCCTTACAGAAATTAAGCGGGGCGGTGGGGGCAC 1941


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Db 1321 CAAATGCTAAGTCTGCTTGTACACGTGTGAAGTCAATGCCAGAGGCCCCAGG 1380
Oy 1381 CAGGCCACCATATTAGTCTGTGGCTGGGCAAGATAAGCATTTCTAATAGAAATCT 1440
Db 1381 CAGGCCACCATATTAGTCTGTGGCTGGGCAAGATAAGCATTTCTAATAGAAATCT 1440
Oy 1441 GCCAATTTTTAAAAAGTAAGTACACGTACAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
Db 1441 GCCAATTTTTAAAAAGTAAGTACACGTACAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
Oy 1501 CTGCCAGCCACATGCACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 CTGCCAGCCACATGCACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Oy 1561 CTGCCAGCCACATGCACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1561 CTGCCAGCCACATGCACACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Oy 1621 TTTCAGCACTAGAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 TTTCAGCACTAGAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Oy 1681 ACCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
Db 1681 ACCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
Oy 1741 GGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
Db 1741 GGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800
Oy 1801 CTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1860
Db 1801 CTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1860
Oy 1861 TGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db 1861 TGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Oy 1921 CCCAGGCGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Db 1921 CCCAGGCGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
Oy 1981 AGCAGGCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Db 1981 AGCAGGCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
Oy 2041 CATGAATTTCTAGACAGACAGAGGCTGATTAATTTGATTAATTTGATTAATTTGATTA 2100
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Oy 2521 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2580
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Oy 2581 GCTTATCAATTAACCTTTTGTAAAAA 2613
Db 2581 GCTTATCAATTAACCTTTTGTAAAAA 2613

RESULT 2
HS118D24/c
LOCUS
DEFINITION
  Human DNA sequence from clone 118D24 on chromosome 1p36.11-36.33.
  Contains part of a novel gene similar to worm genes T08G11.1 and
  C25H3.9, part of a 60S Ribosomal Protein L10 like (pseudo)gene and
  two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2
  (75 kD) (TNF Binding Protein 2, TNFR1, TNFR2, CD120B, TNFR).
  Contains ESTs, STS, GSS, genomic marker DIS434 and a ca repeat
  polymorphism, complete sequence.
ACCESSION
  AL031276
VERSION
  AL031276.1 GI:3947780
KEYWORDS
  HTG: 60S Ribosomal Protein L10; C25H3.9; ca repeat polymorphism;
  CD120B; DIS434; T08G11.1; TNFR1; TNF Binding Protein 2; TNFR2;
  TNFR; TNFR2; Tumor Necrosis Factor Receptor 2.
SOURCE
  Homo sapiens.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
  1 (bases 1 to 115602)
REFERENCE
  Heath, P.
  Submitted (01-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
  UK. E-mail enquiries: humquery@sanger.ac.uk
  Requesters: humquery@sanger.ac.uk
  On Dec 2, 1998 this sequence version replaced gi:3724207.
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  only a small overlap as described above.
  This sequence is the entire insert of clone 118D24. This sequence
  has been finished according to sequence map criteria as follows. An
  attempt is made to resolve all sequencing problems, such as
  compressions and repeats, but not necessarily within known
  annotated human repeat sequence elements (e.g. Alu). Where the
  sequence is ambiguous, there is an annotation using the 'unsure'
  feature key.
  This sequence was generated from part of bacterial clone contigs of
  human chromosome 1, constructed by the Sanger Centre Chromosome 1
  Mapping Group. Further information can be found at
  http://www.sanger.ac.uk/HGP/Chr1
  118D24 is from the library RPC15 constructed at the Roswell Park
  Cancer Institute by the group of Pletier de Jong. For further
  details see http://bacpac.med.buffalo.edu/VECTOR:pcyrc2.
  Location/Qualifiers
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      /db_xref="taxon:9606"
      /chromosome="1"
      /map="p36.11-36.33"
      /clone="RP5-118D24"
      /clone_lib="RPC1-5"
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FEATURES
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  gene
  CDS

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supported by GENSCAN"
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/db_xref="SPTREMBL:O95536"
/translation="QESSPEDHVLCDVCVVDLDDMFDAFMRHREYSKAPEDSSG
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400..677
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678..685
repeat_region
/note="94 copies 2 mer ga 64% conserved"
963..1520
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1677..1797
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1824..2133
repeat_region
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2152..2413
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2418..2569
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2671..2966
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4121..4505
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16370..16674
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18657..18729
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21662..21943
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22857..22987
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24455..24763
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24933..25227
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25238..25548
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25860..26031
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27211..27447
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28213..28252
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29428..29725
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33043..33353
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Query Match

98.5%: Score 2575: DB 9: Length 115602:

Best Local Similarity 99.7%: Pred. No. 0:
Matches 2601: Conservative 0: Mismatches 5: Indels 3: Gaps 2:

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OY 1 TCTTGCTCTGGCTCTCTGGCCCACTGCTCTTTTCCATGTGTGATCTGCATCTTGGGC 60
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Db 104999 TCTTGCTCTGGCTCTCTGGCCCACTGCTCTTTTCCATGTGTGATCTGCATCTTGGGC 104940

OY 61 AGGGTCCCTGGGGCCCACTCTCTGAGCCCGGAGTACCCCGACCCCATCTGTTCTTAA 120
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Db 104939 AGGGTCCCTGGGGCCCACTCTCTGAGCCCGGAGTACCCCGACCCCATCTGTTCTTAA 104880

OY 121 GCAGATTCCTCCCTGCTGGCCATGGAGCCAGTCAATGTCACTGTCAATCTGTAACGTIC 180
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Db 104879 GCAGATTCCTCCCTGCTGGCCATGGAGCCAGTCAATGTCACTGTCAATCTGTAACGTIC 104820

OY 181 TGTAGCAGCTGTGACACAGTCACTGCTCTCTCTCCCAAGCCAGCTTCACATGGAGAC 240
    |||||||
Db 104819 TGTAGCAGCTGTGACACAGTCACTGCTCTCTCTCCCAAGCCAGCTTCACATGGAGAC 104760

OY 241 ACAGATTCACAGCCCTCTGGAGTCCCGAAGAGACAGAGTCCCTTCTCCAAAGAGAA 300
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Db 104759 ACAGATTCACAGCCCTCTGGAGTCCCGAAGAGACAGAGTCCCTTCTCCAAAGAGAA 104700

OY 301 TGTGCTCTTGGGTACAGCTGAGAGACCCAGAGACCTCTGCTGGAGACCGAAGAGAA 360
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Db 104699 TGTGCTCTTGGGTACAGCTGAGAGACCCAGAGACCTCTGCTGGAGACCGAAGAGAA 104640

OY 361 CCCCTGCCCTTGGAGTGCCTGATGCTGGGATGAAGCCCAAGTAAACAGAGCCGGGTGGG 420
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Db 104639 CCCCTGCCCTTGGAGTGCCTGATGCTGGGATGAAGCCCAAGTAAACAGAGCCGGGTGGG 104580

OY 421 CTGTGTCTGAGCCAGAGTGGGCTGAGCCCTGAGAGATGACCTCGAAGGGGCTCTGT 480
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Db 104579 CTGTGTCTGAGCCAGAGTGGGCTGAGCCCTGAGAGATGACCTCGAAGGGGCTCTGT 104520

OY 481 CCTTCAGAGGCCCCACACAGACCTGAGCTCTTTTGGGCCAAGTCTCTCTAGTGC 540
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Db 104519 CCTTCAGAGGCCCCACACAGACCTGAGCTCTTTTGGGCCAAGTCTCTCTAGTGC 104460

OY 541 CTTCCACAGCCGACAGCTCCCTCTGACTGTAGAGCCAAAGAGAGAGAGAGAGTGGGG 600
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Db 104459 CTTCCACAGCCGACAGCTCCCTCTGACTGTAGAGCCAAAGAGAGAGAGAGAGTGGGG 104400

OY 601 AAGCCCTGTGCTCCATGTGTGTCTCTTCCGAAAGCTGCGTGGGCAATGACGTTGGG 660
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Db 104399 AAGCCCTGTGCTCCATGTGTGTCTCTTCCGAAAGCTGCGTGGGCAATGACGTTGGG 104340

OY 661 GCATGCTGGGGCAAGTCCCTGACTCTGTGACGTGCCCGCCGACGCTGACCTGCCAGC 720
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Db 104339 GCATGCTGGGGCAAGTCCCTGACTCTGTGACGTGCCCGCCGACGCTGACCTGCCAGC 104280

OY 721 CTGGCTTCTGAGACCCCTTGGGTTTTTGTGTTGTTGTTGTTGTTGTTGTTCTCC 780
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Db 104279 CTGGCTTCTGAGACCCCTTGGGTTTTTGTGTTGTTGTTGTTGTTGTTGTTCTCC 104220

OY 781 CTTGGGCTCTG-CCAGAGCTGTGGCTTCCAGAAAGCCAGCATCTTTTCTGCAAGGGG 839
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Db 104219 CTTGGGCTCTG-CCAGAGCTGTGGCTTCCAGAAAGCCAGCATCTTTTCTGCAAGGGG 104160

OY 840 CTTTCTGAGAGAGAGATGTGCTGTGATCACCCATGAACAGAGACAGTCTTCAAGCC 899
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Db 104159 CTTTCTGAGAGAGAGATGTGCTGTGATCACCCATGAACAGAGACAGTCTTCAAGCC 104100

OY 900 TGAAGCTGAGATGCGGGATGTCTTGGGGCTCTGTGTAGGAGAGAGTGGACCCCTGT 959
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Db 104099 TGAAGCTGAGATGCGGGATGTCTTGGGGCTCTGTGTAGGAGAGAGTGGACCCCTGT 104040

OY 960 AGGGAACGGGCTCTTCAAGTTAGCTAGAGAGCTTGGAAAGCATCACTCAGGCCAGGT 1019
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Db 104039 AGGGAACGGGCTCTTCAAGTTAGCTAGAGAGCTTGGAAAGCATCACTCAGGCCAGGT 103980

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Db 103919 GGTATGAGATTGAGAGACAGCCTGGCCACATGGTAAACCCCATCTCTACTTAAAAATAC 103860

OY 1140 AGAAATTAGCCGGGCGTGTGGGCGGACCTATAGTCCAGTACTCAGAAAGCTTGAGG 1199
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Db 103859 AGAAATTAGCCGGGCGTGTGGGCGGACCTATAGTCCAGTACTCAGAAAGCTTGAGG 103800

OY 1200 TGGGAAATCGTTTAAACCCCGGAAAGCGAGGTTGCAAGGAGCCGAGATCAGCCCATGCA 1259
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Db 103799 TGGGAAATCGTTTAAACCCCGGAAAGCGAGGTTGCAAGGAGCCGAGATCAGCCCATGCA 103740

OY 1260 CTCCAGCCTGGGCGCAGACGAGAGTCTGTCTCAAAAGAAAAAAGAAAAAAGCACCCT 1319
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OY 1320 CCAATCTTAACTTGTCTCTTTTGTACCATGTGTGAAGTCAAGATGCCAGAGGCCAG 1379
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OY 1380 GCAGGCCACCATATGATGCTGCTGGCTGGCGAGATTAAGCAGCTTCTTAACTAGAAATC 1439
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OY 1440 TGCCAAATTTTTTAAAAAAGTAAGTACACTCAGAGCCCAACAGCAAGCAAGCAAGCAAC 1499
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Db 103561 TGCCAAATTTTTTAAAAAAGTAAGTACACTCAGAGCCCAACAGCAAGCAAGCAAGCAAC 103502

OY 1500 TGTGCCAGCCACATCCCAACCCCCACCTGCATTTGCAACCTCCGCTTCACTCCGCTGT 1559
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Db 103501 TGTGCCAGCCACATCCCAACCCCCACCTGCATTTGCAACCTCCGCTTCACTCCGCTGT 103442

OY 1560 GCTTGGAGCCCCCGGCTCTCTCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1619
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Db 103441 GCTTGGAGCCCCCGGCTCTCTCTCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 103382

OY 1620 TTTTCAGAACTAGAGATGACTGATCTCTGAGCCATCTCTACTTACTTACTGAGCTA 1679
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Db 103381 TTTTCAGAACTAGAGATGACTGATCTCTGAGCCATCTCTACTTACTTACTGAGCTA 103322

OY 1680 GACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1739
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Db 103321 GACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 103262

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OY 1860 ATGGCCTGCTTGAAGCCACTGAACCTGGGATCTCTCTCTCTCTCTCTCTCTCTCTCT 1919
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Db 103141 ATGGCCTGCTTGAAGCCACTGAACCTGGGATCTCTCTCTCTCTCTCTCTCTCTCT 103082

OY 1920 TCCCAAGGCGCAGGGCTGTGCAAGAGGGGAAACAGTGTAGCTTTCGGGAGTTCGGAG 1979
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Db 103081 TCCCAAGGCGCAGGGCTGTGCAAGAGGGGAAACAGTGTAGCTTTCGGGAGTTCGGAG 103022

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OY 2100 CTTGAGCTTGGCAGCTGAACTATTGAGAGGTGGAGAGCCAGCATTTACATGAGAGACA 2159
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Db 102541 CATCACAGGCGAGCGCGGAGGAGCATGATTTGAGAGCTCTGAGGCGCTTGGTCCCT 102482
OY 2520 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2579
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Db 102481 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 102422
OY 2580 TGCCTATATCAATTAACCTGTTGTTTAA 2608
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Db 102421 TGCCTATATCAATTAACCTGTTGTTTAA 102393

RESULT 3
AL355998 122105 bp DNA linear HTG 07-SEP-2001
LOCUS DEFINITION Homo sapiens chromosome 1 clone RP5-1125M11, ** SEQUENCING IN
PROGRAMS ***, in ordered pieces.
ACCESSION AL355998
VERSION AL355998.9 GI:15523662
KEYWORDS HTG: HTGS_PHASE2; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 122105)
Direct Submission
Submitted (05-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 7, 2001 this sequence version replaced gi:13897067.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dj1125M11
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing Vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 121044 bases at least Q40
Consensus quality: 121310 bases at least Q30
Consensus quality: 121451 bases at least Q20
Insert size: 122105; sum-of-contigs
Insert size: 142339; 6.8% error; agarose-fp
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* NOTE: This is a 'working draft' sequence.
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* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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AUTHORS	Unpublished		
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REFERENCE
AUTHORS
Direct Submission
Submitted (10-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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TITLE
JOURNML
COMMENT
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7139786.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L6342
Center clone name: 353.D.18

----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
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Insert size: 185477; sum-of-ctrls
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-ctrls

NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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QY      1500 TCTGCAAGCAGATGCAACCCCGCAAGCTGCAATTTGCAACCTTCGCGCTTCACTGCGGTGT 1559
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QY	1620	TTTTAGGAACATGAGATGACGATCCTCGTAGCCATCTCCTACCTACGACGCTA	1679
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Db	145718	TCTTGTGTGTGCGCTGTGTGTTGGCTGTCTGTTGGGTGTGTGTAGCCAAAGTGTAAATTGA	145778
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QY	2520	TGCTGTGTGTGTGATGCCAAGACAAATGAAGTTTGCACCTGTATGTGACGACGACATTC	2579
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DEFINITION	AX333705	PAT 09-JAN-2002
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VERSION	AX333705.1	
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ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.	
TITLE	Cancer gene determination and therapeutic screening using signature gene sets	
JOURNAL	Patent: WO 01946629-A 4/14 13-DEC-2001: Avalon Pharmaceuticals (US)	
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QY	277	CAGTCCCTCTTCCAGGAGGAAATGTGCTTTCGCTACAGCTGAGAGCCAGGAC	336	
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QY	337	CTGCTGGGAGACACGAGAGAGAACCCCTGCCCCCTTGGAGTGCCTGATGCTGGATGAAG	396	
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QY	397	CCGAGTTAACCAAGGCGGTGTGGGCTGTGTGTAGCCCAAGTGGGCGTGAACCTGGCAG	456	
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QY	457	ATGACCTCGAAGGAGGCGCTGTCTTCCAGGCGCCACACAGTGAAGACTGAGGCTCT	516	
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QY	517	TTCTGGGCCAAGTTCCTCTAGTGCCCTCAGAGCGGAGCCTCCCTCGACTGCAGGCC	576	
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QY	577	AAGAGAGAGGACGAGGTGGGGAACCCCTGCTGCCATGGTGTGCCCTTGGGAAG	636	
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QY	697	CCCCGCCACAGCTGCACCTGACCAGCCTGGCTTCTGGAGACCCTTGGGTTTTTGTGTTTG	756	
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BASE COUNT
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Matches 2502: Conservative 0: Mismatches 15: Indels 0: Gaps 0:
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QY	1597	CCACACCATCTCCTTTTCAGGGAATTTTCAGAGAACTGAGATGACTGATCTCTGAGCCAT	1656
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Schreiber,S., Hampe,J. and Mascheretti,S.		
JOURNAL	Diagnostic use of polymorphisms in the gene coding for the tnfr		
FEATURES	receptor II and method for detecting non-responders to anti-tnfr		
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ACCESSION	AX348018		
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KEYWORDS	.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Schreibler, S., Hampe, J. and Mascheretti, S.		
	Diagnostic use of polymorphisms in the gene coding for the tnfr		
	receptor II and method for detecting non-responders to anti-tnfr		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
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JOURNAL	Diagnostic use of polymorphisms in the gene coding for the tnfr					
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OY	277	CAGGTCCCTTCTCAAGAGGAATGTGCTTGGTCCAGCTGAGAGGAGCCAGAGAC	336		
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VERSION		M32315.1	GI:189185
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REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS		Smith,C.A., Davis,T., Anderson,D., Solam,L., Beckmann,M.P., Jerry,R., Dover,S.K., Cosman,D. and Goodwin,R.G.	
TITLE		A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins	
JOURNAL MEDLINE		Science 248 (4958), 1019-1023 (1990)	
PUBMED		90260639	
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3492)
 Dembic,Z., Loetscher,H., Gubler,U., Pan,Y.C., Lahm,H.W., Gentz,R.,
 Brockhaus,M. and Lesslauer,W.
 Two human TNF receptors have similar extracellular, but distinct
 intracellular, domain sequences
 Cytokine 2 (4), 231-237 (1990)
 91370690
 196549
 GenBank staff at the National Library of Medicine created this
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 This sequence comes from Figure 1.
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FEATURES
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QY	2257	AGGAGTTTGAGGCTGCAGGAGCTATGATCGCCCACTACCTCAGCCCTGAGC	2310
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DEFINITION			
ACCESSION			
VERSION			
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JOURNAL			
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BASE COUNT			
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HUMTNFR1I 2394 bp mRNA linear PRI 03-SEP-1994

LOCUS

Human tumor necrosis factor receptor II (TNFR1I) mRNA, complete cds.

DEFINITION

Accession M55994.1 GI:339757

VERSION

Keywords glycoprotein; nerve growth factor receptor related; transmembrane protein; tumor necrosis factor receptor; tumor necrosis factor receptor II.

SOURCE

Human histiolytic lymphoma cell line U937, CDNA to mRNA.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 2394)
Kohno,T., Brewer,M.T., Baker,S.L., Schwartz,P.E., King,M.W., Hale,K.K., Squires,C.H., Thompson,R.C. and Vannice,J.L. A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor

TITLE

JOURNAL MEDLINE PUBMED 91045991 2172983

FEATURES

source

gene

CDS

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ACCESSION	Sequence 2 from patent US 6232446.
VERSION	ARI52033
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SOURCE	.
ORGANISM	. Unknown.
REFERENCE	Unknown. Unclassified.
AUTHORS	1 (bases 1 to 2224)
TITLE	Wallach,D., Blyda,J., Beletsky,I., Mett,I. and Engelmann,H.
JOURNAL	TNF ligands Patent: US 6232446-A 2 15-MAY-2001;
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VERSION A78517.1 GI:6090179
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ORGANISM
REFERENCE 1 (bases 1 to 2253)
AUTHORS Mett, I. and Wallach, D.
TITLE TNF LIGANDS
JOURNAL Patent: EP 0585939-A 1 09-MAR-1994;
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Search completed: December 6, 2002, 03:47:59
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CC format directly from WIPD at
ftp.wipo.int/pub/published_pcl_sequences.

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

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Searched: 2185239 segs, 112599159 residues

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Listing first 45 summaries

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10	1171	44.8	2394	22 AAC83951	Human 40 kDa TNF 1
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19	245.2	9.4	618	22 AAK62220	Human immune/haema
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21	244	9.3	27154	22 AAL05708	Human reproductive
22	243.2	9.3	2932	13 AAQ25388	TXA2 receptor gene
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25	243.2	9.3	2932	24 ABR83654	DNA encoding novel
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PR	30-NOV-1998; 98US-0110268.	
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PI		
PI	Spolia LD;	
DR	WPI: 2000-412362/35.	
XX		
XX		
PT	Identifying individuals at risk of developing osteoporosis comprises	
PT	assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene	
XX	in a DNA sample from an individual -	
PS	Claim 2; Page 17-18; 21pp; English.	
XX		
CC	The present sequence comprises exon 10 of the human tumour necrosis	
CC	factor alpha receptor 2 (TNFR2) gene. The sequence contains three	
CC	polymorphic sites. By determining the genotype of an individual it is	
CC	possible to identify those at risk of osteoporosis, which is	
CC	characterised by low bone density and fragile bones, later in life. Those	
CC	at greatest risk are those who possess allele 1, which is the rarest	
CC	allele. This is particularly useful as many cases of osteoporosis go	
CC	undetected at present.	
XX		
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OY	301 TGTGCTTTTCGCTCACAGCTGGAGACGCCAGAGACCTGTGTGGGAGCACCGAAGAGAAG	360
DB	301 TGTGCTTTTCGCTCACAGCTGGAGACGCCAGAGACCTGTGTGGGAGCACCGAAGAGAAG	360
OY	361 CCCCGTCCCTTGGAGTGCCTGATGCTGGATGGAAGCCAGTTAAACAGGGCCGGGTGGG	420
DB	361 CCCCGTCCCTTGGAGTGCCTGATGCTGGATGGAAGCCAGTTAAACAGGGCCGGGTGGG	420
OY	421 CTGTGCTGTACCAAGTGTGGCTCAGCCCTGCGACAGATGACCTTCCGAAGGGCCCTTGGT	480
DB	421 CTGTGCTGTACCAAGTGTGGCTCAGCCCTGCGACAGATGACCTTCCGAAGGGCCCTTGGT	480
OY	483 CTTTCCAGGCCCCCACTAGAGACTGTGAGGCTTTTCTGGGCCAATTCCTCTAGTGC	540
DB	483 CTTTCCAGGCCCCCACTAGAGACTGTGAGGCTTTTCTGGGCCAATTCCTCTAGTGC	540

1621 TTCAGAACTAGAGATGACTGAGTCCCGAGGCATCTGCTACCTACCTACGCTAG 1680
1621 TTTCAGAACTAGAGATGACTGAGTCCCGAGGCATCTGCTACCTACCTACGCTAG 1680
1681 ACCCTCTCTCCCTCCAGAGAGGGGTGGGTTCTCTTCCCTCCACTCCACCTCAATTCCTG 1740
1681 ACCCTCTCTCTCCCTCCAGAGAGGGGTGGGTTCTCTTCCCTCCACTCCACCTCAATTCCTG 1740
1741 GGGCCCAAGGGGCTCCCTCCACTTTGGTACATGAGCCAGTGTATCCCAAGTCCAGT 1800
1741 GGGCCCAAGGGGCTCCCTCCACTTTGGTACATGAGCCAGTGTATCCCAAGTCCAGT 1800
1801 CTGTGTCTGCTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
1801 CTGTGTCTGCTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
1861 TGGCTCTGCTTGAAGCCACTGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
1861 TGGCTCTGCTTGAAGCCACTGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
1921 CCCAGGGCCAGGGCCCTTGGAGAGGGGAACAGTGTAGCTTGGCCGATTTCTGGAGAGA 1980
1921 CCCAGGGCCAGGGCCCTTGGAGAGGGGAACAGTGTAGCTTGGCCGATTTCTGGAGAGA 1980
1981 AGCAGGTTGAGGGGCTCTGGAAGGCTCAGTCTCAGAGCATGGGGATTAAGAGAGAG 2040
1981 AGCAGGTTGAGGGGCTCTGGAAGGCTCAGTCTCAGAGCATGGGGATTAAGAGAGAG 2040
2041 CATGAATTTGCTAGAGAGAGAGAGGGGAGGAGTGAATTTGTTGATTAATTCACCTGAGC 2100
2041 CATGAATTTGCTAGAGAGAGAGAGGGGAGGAGTGAATTTGTTGATTAATTCACCTGAGC 2100
2101 TTGACGCTTGGCAGCTGAATTTGGAGGCTGGAGAGCCGACCTTACATGAGAGAGA 2160
2101 TTGAGCTTGGCAGCTGAATTTGGAGGCTGGAGAGCCGACCTTACATGAGAGAGA 2160
2161 GAAGGCTTTTCCACCTGGATCAAGATGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2161 GAAGGCTTTTCCACCTGGATCAAGATGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2221 GACTCAGAGAGCTGAGGGAGAGATCACTGGAGCCGAGAGTGTAGAGCTGAGAGAGCT 2280
2221 GACTCAGAGAGCTGAGGGAGAGATCACTGGAGCCGAGAGTGTAGAGCTGAGAGAGCT 2280
2281 ATGATCGCGCCACTACCTCCAGCTTGAGCAACAGAGTGAAGAGCTGCTGCTTAAAGAAA 2340
2281 ATGATCGCGCCACTACCTCCAGCTTGAGCAACAGAGTGAAGAGCTGCTGCTTAAAGAAA 2340
2281 ATGATCGCGCCACTACCTCCAGCTTGAGCAACAGAGTGAAGAGCTGCTGCTTAAAGAAA 2340
2341 AAAAAAGTCAGACTGCTGGAGCTGGCAGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
2341 AAAAAAGTCAGACTGCTGGAGCTGGCAGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2400
2401 ATGATGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
2401 ATGATGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460
2461 ATGATGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
2461 ATGATGAGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520
2521 GGT 2580
2521 GGT 2580
2581 GCTTATCAATAAACCTGTTTGTTTTAAAAAAA 2613
2581 GCTTATCAATAAACCTGTTTGTTTTAAAAAAA 2613

RESULT 2
ABK83997
ID ABK83997 standard; cDNA: 3683 BP.

ABK83997:
14-AUG-2002 (first entry)
Human cDNA differentially expressed in granulocytic cells #568.
Human; ss: granulocytic cell; DNA chip: bacterial infection;
viral infection; parasitic infection; protozoal infection;
fungal infection; sterile inflammatory disease; psoriasis;
rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
cardiac reperfusion injury; renal reperfusion injury; AIDS;
adult respiratory distress syndrome; inflammatory bowel disease;
Crohn's disease; ulcerative colitis; periodontal disease;
granulocyte activation; chronic inflammation; allergy.
Homo sapiens.
MO200228999-A2.
11-APR-2002.
03-OCT-2001: 2001MO-US30821.
03-OCT-2000: 2000US-237189P.
(GENE-) GENE LOGIC INC.
Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
WPI: 2002-435328/46.
Detecting granulocyte activation by detecting differential expression
of genes associated with granulocyte activation, which serves as
diagnostic markers that is useful for monitoring disease states and
drug toxicity
Claim 1: SEQ ID No 568: 114pp: English.
The invention relates to detecting (M1) granulocyte (GC) activation
(GCA), by detecting the level of expression of gene(s) (Gs) identified by
DNA chip analysis as given in the specification, and comparing
the expression level to an expression level in an unactivated
GC, where differential expression of Gs is indicative of GCA.
Also included are modulating (M2) Gs by contacting GC with an agent
that alters the expression of at least one gene in Gs; (2) screening (M3)
for an agent capable of modulating GCA or an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease using the
GC gene expression profile; (3) detecting (M4) an inflammation (especially
chronic) in a tissue, an allergic response in a subject, exposure of a
subject to a pathogen or sterile inflammatory disease, by detecting the
level of expression in a sample of the tissue of gene(s) from Gs, where
the level of expression of the gene is indicative of inflammation;
(4) treating (M5) an inflammation (especially chronic) or in a tissue,
an allergic response in a subject, exposure of a subject to a pathogen
or sterile inflammatory disease, by contacting a tissue having
inflammation with an agent that modulates the expression of gene(s)
from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
modulating Gs; M3 is useful for screening an agent capable of modulating
GCA preferably in an inflammation in a tissue; M4 is useful for
detecting an inflammation (especially chronic) in a tissue, an allergic
response in a subject, exposure of a subject to a pathogen or sterile
inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
reperfusion injury, AIDS, adult respiratory distress syndrome,
inflammatory bowel disease, Crohn's disease, ulcerative colitis,
periodontal disease; also bacterial infection, viral infection,
parasitic infection, protozoal infection, fungal infection and M5 is
useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic

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Db 3207 GCCCAGCCATTACCATGAGACAGAAAGCGTTTTCACCTGGAAATCAAGATGTCAGACT 3266
Qy 2197 GCGTGGCTGACGAGTACGTCACCTGTACTGAGAGGCGTGAAGGAGATGCTGAGACCC 2256
Db 3267 GCGTGGCTGACGAGTACGTCACCTGTACTGAGAGGCGTGAAGGAGATGCTGAGACCC 3336
Qy 2257 AGGATTTTGAAGCTTCGACGAGCTATGATCGCCGACCTACACCTCAGCTGAGCAAGAGA 2316
Db 3327 AGGATTTTGAAGCTTCGACGAGCTATGATCGCCGACCTACACCTCAGCTGAGCAAGAGA 3386
Qy 2317 GTGAGACCCCTGCTCTTAAACAAAAAAATCACTGAGCTGCGGAGCTGCGCAGTTTCTG 2376
Db 3387 GTGAGACCCCTGCTCTTAAACAAAAAAATCACTGAGCTGCGGAGCTGCGCAGTTTCTG 3446
Qy 2377 CCCACATTGACCCACATGAGACATGATGAGAGCGACCTGCCCCGGTGGAGACAGCTT 2436
Db 3447 CCCACATTGAGACCCACATGAGACATGATGAGAGCGACCTGCCCCGGTGGAGACAGCTT 3506
Qy 2437 GCGAGAACCTTCAGGCTTTCCTTGGCATCAGAGGCGAGAGCCGGAAACCATTTTGGAG 2496
Db 3507 GCGAGAACCTTCAGGCTTTCCTTGGCATCAGAGGCGAGAGCCGGAAACCATTTTGGAG 3566
Qy 2497 ACTCTGAGGGGCTTGGTTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2556
Db 3567 ACTCTGAGGGGCTTGGTTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3626
Qy 2557 CACTGTATGCTGAGAGCGCATTCCTGCTTATCAATAAAGCTGTTTGTAAAAA 2613
Db 3627 CACTGTATGCTGAGAGCGCATTCCTGCTTATCAATAAAGCTGTTTGTAAAAA 3683

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RESULT 3

ABL5877
ID ABL5877 standard; DNA: 3683 BP.

AC ABL5877;

DT 15-MAY-2002 (first entry)

DE Lung cancer related gene sequence SEQ ID NO:4214.

XX Human: cancer: colon; breast; ovary; oesophagus; kidney; thyroid;

KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KM cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;

XX gene; ds.

OS Homo sapiens.

XX

XX

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XX

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XX

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PR 27-SEP-2000: 2000US-235720P.
PR 27-SEP-2000: 2000US-235840P.
PR 27-SEP-2000: 2000US-235863P.
PR 28-SEP-2000: 2000US-236028P.
PR 28-SEP-2000: 2000US-236032P.
PR 28-SEP-2000: 2000US-236033P.
PR 28-SEP-2000: 2000US-236034P.
PR 28-SEP-2000: 2000US-236109P.
PR 28-SEP-2000: 2000US-236111P.
PR 29-SEP-2000: 2000US-236842P.
PR 29-SEP-2000: 2000US-237172P.
PR 02-OCT-2000: 2000US-237173P.
PR 02-OCT-2000: 2000US-237278P.
PR 02-OCT-2000: 2000US-237294P.
PR 02-OCT-2000: 2000US-237295P.
PR 02-OCT-2000: 2000US-237316P.
PR 03-OCT-2000: 2000US-237425P.
PR 03-OCT-2000: 2000US-237598P.
PR 03-OCT-2000: 2000US-237604P.
PR 03-OCT-2000: 2000US-237606P.
PR 03-OCT-2000: 2000US-237608P.
PR 01-NOV-2000: 2000US-244867P.
PR 01-NOV-2000: 2000US-245084P.

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(AVAL-) AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Soppet DR, Weaver Z;

XX MPI: 2002-188264/24.

PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -

XX Claim 1: SEQ ID 4214; 44pp: English.

XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (1) of a signature gene set, where (1)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL51664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer.
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilms tumour.

XX Sequence 3683 BP; 781 A; 1098 C; 1086 G; 718 T; 0 other:

XX Query Match 95.48; Score 2493; DB 24; Length 3683;

XX Best Local Similarity 99.48; Pred. No. 0;

XX Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 97 GACCCACCCACCATCTGTGCTTGTAGCAGATTCCTCCCTGCTGCGCATGAGACCCAGCTC 156

Db 1167 GAGGCCCGGGCCAGCACCAGGAGCTCAGATTCTTCCCTGTGGCCATGGAGCCAGCTC 1226

Qy 157 AATGTACCTTCATCGTGAACGCTGTAGAGCTGTGACCAACAGCTACAGTCTCTCC 216

Db 1227 AATGTACCTTCATCGTGAACGCTGTAGAGCTGTGACCAACAGCTACAGTCTCTCC 1286

Qy 217 CAAGCCAGCTTCACAAATGGAGACACAGATTCAGCCCTCGAGTCCCGAAGACGAG 276

Db 1287 CAAGCCAGCTTCACAAATGGAGACACAGATTCAGCCCTCGAGTCCCGAAGACGAG 1346

QY	277	CAGTCCCTTCTTCCAGAGAGAAATGTGCTTTTCGCTCACAGCTGAGACGCCACAGAC	336
Db	1347	CAGGTCCCTTCTCTCAAGAGAGAAATGTGCTTTTCGCTCACAGCTGAGACGCCACAGAC	1408
QY	337	CTGCTGGGAGACACAGGAAGAAACCCCTCTGCCCCCTTGGAGTGGCTGATCTCTGGATGAG	396
Db	1407	CTGCTGGGAGACACAGGAAGAAACCCCTCTGCCCCCTTGGAGTGGCTGATCTCTGGATGAG	1466
QY	397	CCCACTTAACAGGCCGGGTGTGGCTGTGTGTGTAGCCAAAGTGGCTGAGCCCTGGCAGG	456
Db	1467	CCCACTTAACAGGCCGGGTGTGGCTGTGTGTGTGTAGCCAAAGTGGCTGAGCCCTGGCAGG	1526
QY	457	ATGACCCCTGGCAAGGGGCCCGTGGCTCTTCAGGCCCCCCCACTATGAACTGTGAGGCTCT	516
Db	1527	ATGACCCCTGGCAAGGGGCCCGTGGCTCTTCAGGCCCCCCCACTATGAACTGTGAGGCTCT	1588
QY	517	TTCTGGGCAAGTTCTCTAGTGCCTTCACAGCCGACGCTCCCTGTGACCTGTGAGGCC	576
Db	1587	TTCTGGGCAAGTTCTCTAGTGCCTTCACAGCCGACGCTCCCTGTGACCTGTGAGGCC	1648
QY	577	AAGACACAGGACACGAGTTGGGAAAGCCTGTGCTGCTGCTGATGTGTCTCTGTGAGAG	636
Db	1647	AAGACACAGGACACGAGTTGGGAAAGCCTGTGCTGCTGCTGATGTGTCTCTGTGAGAG	1706
QY	637	CTGTCTGGGATGAGAGTTTCGGGGCATGCTGGGGCAAGTCCCTGACTCTGTGAGCTG	696
Db	1707	CTGTCTGGGATGAGAGTTTCGGGGCATGCTGGGGCAAGTCCCTGACTCTGTGAGCTG	1766
QY	697	CCCCGCCAGCTGCACCTGCCAGCTGTGCTTCTGAGACCCCTTGGGTTTGTGTGTGTG	756
Db	1767	CCCCGCCAGCTGCACCTGCCAGCTGTGCTTCTGAGACCCCTTGGGTTTGTGTGTGTG	1826
QY	757	TTTGT	816
Db	1827	TTTGT	1886
QY	817	CAGCATCCTTTTCTGACAGAGGGCTTTCTGTGAGAGGAGGGATGCTGCCATCAACCAT	876
Db	1887	CAGCATCCTTTTCTGACAGAGGGCTTTCTGTGAGAGGAGGGATGCTGCCATCAACCAT	1946
QY	877	GAAACACAGAGACAGTGTCTCAAGGCTGTAGAGGTGAGACATGGGGATGCTGCTGGGCTCTGTG	936
Db	1947	GAAACACAGAGACAGTGTCTCAAGGCTGTAGAGGTGAGACATGGGGATGCTGCTGGGCTCTGTG	2006
QY	937	TAGGAGAGAGGTGGACACCTGTAGGGAACGGGGTCTCTCAAGTTAGCTCAGAGAGCTTG	996
Db	2007	TAGGAGAGAGGTGGACACCTGTAGGGAACGGGGTCTCTCAAGTTAGCTCAGAGAGCTTG	2066
QY	997	GAAAGCATCACCTCAGGCCAAGGTGACAGTGGCTCAGCCTATGATCCACAGACCTTTGGGAG	1056
Db	2067	GAAAGCATCACCTCAGGCCAAGGTGACAGTGGCTCAGCCTATGATCCACAGACCTTTGGGAG	2126
QY	1057	GCTAGAGCGGGTGGATACCTGTAGAGTTAGAGAGTTGAGACACAGCCTGGCCCAACATGGTAA	1116
Db	2127	GCTAGAGCGGGTGGATACCTGTAGAGTTAGAGAGTTGAGACACAGCCTGGCCCAACATGGTAA	2186
QY	1117	AACCCATCTCTACTAATAAATACAGAAATTAGCCGGGCTGTGTGGCGGGACCTATATGCT	1176
Db	2187	AACCCATCTCTACTAATAAATACAGAAATTAGCCGGGCTGTGTGGCGGGACCTATATGCT	2246
QY	1177	CCACTTACTAGAAAGCCTGTAGGCTGTGGGAATGTTTGAACCCGGGACAGGAGTTGACG	1236
Db	2247	CCACTTACTAGAAAGCCTGTAGGCTGTGGGAATGTTTGAACCCGGGACAGGAGTTGACG	2306
QY	1237	GGAGCCAGATTCAGGCACTGCACTCCACCTGGGGGAGAGAGCAGAGTGTCTCTCAA	1296
Db	2307	GGAGCCAGATTCAGGCACTGCACTCCACCTGGGGGAGAGAGCAGAGTGTCTCTCAA	2366
QY	1297	AGAAAAAAGAGACAGCCGCTTCCAAATGCTTAAGTTGCTTTTGTACATGGTGTGAA	1356
Db	2367	AGAAAAAAGAGACAGCCGCTTCCAAATGCTTAAGTTGCTTTTGTACATGGTGTGAA	2426

QY	1357	AGCAGATGCCCCAGAGGGGCCACAGGCCACCAATATTCAGTGTGTGGCTGGCCAGAGA	1416
Db	2427	AGTCAGATGCCCCAGAGGGGCCAGGGCCAGGCCACACATATTCAGTGTGTGGCTGGCCAGAGA	2486
QY	1417	TAACGACATCTTAACAGAAATCTGGCAATTTTTAAAAAATAAGTACATCAGGCCA	1476
Db	2487	TAACGACATCTTAACAGAAATCTGGCAATTTTTAAAAAATAAGTACATCAGGCCA	2546
QY	1477	ACAAGCCAAGCAACAAAGCCAAACTGTGCCAGCCACATCCAAACCCCCACACTGCCATTTGC	1536
Db	2547	ACAAGCCAAGCAACAAAGCCAAACTGTGCCAGCCACATCCAAACCCCCACACTGCCATTTGC	2606
QY	1537	ACCCCTCCGCTTACACTCCGGTGTGGCTGGAGCCCCGGCCGCTCCTTCCTTGTGCTCTAG	1596
Db	2607	ACCCCTCCGCTTACACTCCGGTGTGGCTGGAGCCCCGGCCGCTCCTTCCTTGTGCTCTAG	2666
QY	1597	CCACACATCTCTCTTCAGGGAATTTTCAGAACTAGAGATGACAGTCTCTGTAGCCAT	1656
Db	2667	CCACACATCTCTCTTCAGGGAATTTTCAGAACTAGAGATGACAGTCTCTGTAGCCAT	2726
QY	1657	CTCTCTACTCCCTACCTCAACCCCTAAGACCCCTCCCTCTCCCCAGAGGGGTGGTCTCTTC	1716
Db	2727	CTCTCTACTCCCTACCTCAACCCCTAAGACCCCTCCCTCTCCCCAGAGGGGTGGTCTCTTC	2786
QY	1717	CCCACTCCCAACCTTCAATTCCTGGAGCCCAACAGGGCGCCCTGCCACTTGTGTACATG	1776
Db	2787	CCCACTCCCAACCTTCAATTCCTGGAGCCCAACAGGGCGCCCTGCCACTTGTGTACATG	2846
QY	1777	GCCAGTGTATCCCAAGTGTCCACAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1836
Db	2847	GCCAGTGTATCCCAAGTGTCCACAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2906
QY	1837	TGTAGCAAGGTGGGTAAAGTTGAATGGCCCTGCTTGAAGCCCTGACACTGGGATTCCTC	1896
Db	2907	TGTAGCAAGGTGGGTAAAGTTGAATGGCCCTGCTTGAAGCCCTGACACTGGGATTCCTC	2966
QY	1897	CCCATTAGAGTACGCTTCCCTCCCAAGGGCCAGGGCCCTGTGACAGGGGAAACCAGTGT	1956
Db	2967	CCCATTAGAGTACGCTTCCCTCCCAAGGGCCAGGGCCCTGTGACAGGGGAAACCAGTGT	3026
QY	1957	ACCCCTGGCCGATTCCTGGAGGAAGGAGTGTGAGGGGCTCCTGGAAGGCTCAACTCTCA	2016
Db	3027	ACCCCTGGCCGATTCCTGGAGGAAGGAGTGTGAGGGGCTCCTGGAAGGCTCAACTCTCA	3086
QY	2017	GGAGCATGGGGTAAAGGAGAAAGGCATGAATTTGTCTAGCAGAGCAGGGGCGAGGTGATA	2076
Db	3087	GGAGCATGGGGTAAAGGAGAAAGGCATGAATTTGTCTAGCAGAGCAGGGGCGAGGTGATA	3146
QY	2077	AATTTGTAATAATTCACACTGGACTTGTGAGCTTGTGAGCTGAACATTTTGGAGGGTGGAGA	2136
Db	3147	AATTTGTAATAATTCACACTGGACTTGTGAGCTTGTGAGCTGAACATTTTGGAGGGTGGAGA	3206
QY	2137	GCCAGCCATTACATGTGAGAACAAAGAGGTTTTCCACCTCTGGAAATCAAGATGTACAGCT	2196
Db	3207	GCCAGCCATTACATGTGAGAACAAAGAGGTTTTCCACCTCTGGAAATCAAGATGTACAGCT	3266
QY	2197	GGCTGGCTGCACTGACGTGCACCTGTACTCAGAGAGCTGTAGGGGAGATCACTGGAGCCC	2256
Db	3267	GGCTGGCTGCACTGACGTGCACCTGTACTCAGAGAGCTGTAGGGGAGATCACTGGAGCCC	3326
QY	2257	AGGAGTTTGAGGCTGCAGCGAGCTGTGATTCGGCCACTACACTCAGCCCTGAGCAACGA	2316
Db	3327	AGGAGTTTGAGGCTGCAGCGAGCTGTGATTCGGCCACTACACTCAGCCCTGAGCAACGA	3386
QY	2317	GTGAGACCTGTCTTTAAAGAAAAAAAAGTCAAGACTGTGTGGGACTGTGGCCAGGTTTTCTG	2376
Db	3387	GTGAGACCTGTCTTTAAAGAAAAAAAAGTCAAGACTGTGTGGGACTGTGGCCAGGTTTTCTG	3446
QY	2377	CCCAATTGGAGCCCAATGAGAGATAATGTGAGAGGCCACCTGCCCTGTGTGAGACATCTCT	2436
Db	3447	CCCAATTGGAGCCCAATGAGAGATAATGTGAGAGGCCACCTGCCCTGTGTGAGACATCTCT	3506
QY	2437	GGAGAACCTTAGGCTTCTTGTGGATCAGAGGGCAGACCCGGGAAGCGATGAATTTTGGAG	2496

|||||
DB 3507 GGGAGAACTCAAGCTTCTTGGCATCAAGGCGAGACCCGGAAGCATATTGGAG 3566
OY 2497 ACTCTGTGGGCGCTTGTTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 2556
DB 3567 ACTCTGTGGGCGCTTGTTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 3626
OY 2557 CACTGTATCTGAGCGCATCTCTTATCAATTAACCTTTTGTAAAAA 2613
DB 3627 CACTGTATCTGAGCGCATCTCTTATCAATTAACCTTTTGTAAAAA 3683
RESULT 4
ID ABK33465 standard; DNA; 3683 BP.
XX
AC ABK33465;
XX
DT 23-APR-2002 (first entry)
XX
DE Human TNF receptor II gene.
XX
XX Human: anti-tumour necrosis factor receptor II; TNF receptor II;
KW chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW inflammatory disorder; chronic disease; receptor; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 90..1475
FT sig_peptide /*tag= a
FT product= "TNF receptor II"
FT mat_peptide /*tag= b
FT 156..1472
FT /*tag= c
XX
PN EPI172444-A1.
XX
PD 16-JAN-2002.
XX
PE 10-JUL-2000: 2000EP-0114786.
XX
PR 10-JUL-2000: 2000EP-0114786.
XX
PA (COMA-) COMARIS RES INST GMBH.
XX
P1 Schreiber S, Hampe J, Mascheretti S;
XX
DR WPI: 2002-156651/21.
XX
DR P-PSDB: AAU75172.
XX
PT Detecting non-responders to anti-human necrosis factor therapy,
PT comprises testing an individual for homozygosity for a single
PT nucleotide polymorphism in the gene coding for the tumour necrosis
PT factor receptor II -
XX
PS Disclosure: Page 23-27: 45pp: English.
XX
CC The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC Met156Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC infliximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC encodes for human TNF receptor II.
XX
SO Sequence 3683 BP: 781 A; 1098 C; 1086 G; 718 T; 0 other;

Query Match 95.4%; Score 2493; DB 24; Length 3683;
Best Local Similarity 99.4%; Pred. No. 0; Mismatches 15; Indels 0; Gaps 0;
Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
OY 97 GACCCCAACCCATCTTGTCTTACAGATTCCTCCCTGTGGCCATGGAGCCAGTC 156
DB 1167 GAGGCCCGGCGCAGCAGCGGAGAGTCAGATTCCTCCCTGTGGCCATGGAGCCAGTC 1226
OY 157 AATGTACCTGCATGTCAGAGTCGTGTAGAGCTGTGACACAGCTACAGTCTCTCC 216
DB 1227 AATGTACCTGCATGTCAGAGTCGTGTAGAGCTGTGACACAGCTACAGTCTCTCC 1286
OY 217 CAAGCCACCTCCACAAATGGAGACACAGATTCAGACCCCTGGAGTCCCGAAGAGCAG 276
DB 1287 CAAGCCACCTCCACAAATGGAGACACAGATTCAGACCCCTGGAGTCCCGAAGAGCAG 1346
OY 277 CAGGTCCCTCTCCAGAGGAATGTGCTTTCGTGACAGCTGAGAGCCAGAGACC 336
DB 1347 CAGGTCCCTCTCCAGAGGAATGTGCTTTCGTGACAGCTGAGAGCCAGAGACC 1406
OY 337 CTGCTGGGAGACACCGAAGAGACCCCTGCTGTGAGTGGCTATGTGGATGAAG 396
DB 1407 CTGCTGGGAGACACCGAAGAGACCCCTGCTGTGAGTGGCTATGTGGATGAAG 1465
OY 397 CCAGATTACCAAGCCGGTGTGGCTGTGTCAGCCAAAGTGGGCTGAGCCCTGGCAGG 456
DB 1467 CCAGATTACCAAGCCGGTGTGGCTGTGTCAGCCAAAGTGGGCTGAGCCCTGGCAGG 1526
OY 457 ATGACCCCTGCGAAGGGGCGCTGCTCCAGAGCCCGCCACCACTAGAGACTGTAGGCTCT 516
DB 1527 ATGACCCCTGCGAAGGGGCGCTGCTCCAGAGCCCGCCACCACTAGAGACTGTAGGCTCT 1586
OY 517 TTCTGGGCAAGTCTCTAGTGCCTTCACAGACCGCAGCTCCCTGTGACCTGACAGCC 576
DB 1587 TTCTGGGCAAGTCTCTAGTGCCTTCACAGACCGCAGCTCCCTGTGACCTGACAGCC 1646
OY 577 AAGAGCAGAGGACGAGTGGGGAAGCCCTGTGCTGCATAGTGTGCTCTGGAAG 636
DB 1647 AAGAGCAGAGGACGAGTGGGGAAGCCCTGTGCTGCATAGTGTGCTCTGGAAG 1706
OY 637 GCTGGTGGGATGAGAGTTCGGGGCATGCTGGGGCAATCCCTGACATCTGTGACCTG 696
DB 1707 GCTGGTGGGATGAGAGTTCGGGGCATGCTGGGGCAATCCCTGACATCTGTGACCTG 1766
OY 697 CCGCGCCAGCTGACCTGCGCAGCTGTGAGAGCCCTTGGGTTTGTGTGTTG 756
DB 1767 CCGCGCCAGCTGACCTGCGCAGCTGTGAGAGCCCTTGGGTTTGTGTGTTG 1826
OY 757 TTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 816
DB 1827 TTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1886
OY 817 CAGCATCTTTTGTGAGAGGGGCTTGTGAGAGAGAGATGTGCCGAGTCAACCAT 876
DB 1887 CAGCATCTTTTGTGAGAGGGGCTTGTGAGAGAGAGATGTGCCGAGTCAACCAT 1946
OY 877 GAAGAGAGGACATGCTCTAGAGCTGAGAGCTGCGGATGTCTCTGGGCTCTGTG 936
DB 1947 GAAGAGAGGACATGCTCTAGAGCTGAGAGCTGCGGATGTCTCTGGGCTCTGTG 2006
OY 937 TAGGAGAGAGTGGCAGCCCTGTAGGGAAGGGGGTCTTCAAGTATAGTCAAGAGGCTTG 996
DB 2007 TAGGAGAGAGTGGCAGCCCTGTAGGGAAGGGGGTCTTCAAGTATAGTCAAGAGGCTTG 2066
OY 997 GAAAGCATCACTCAGGCGAGTGTGAGTGTACAGCTATGATCCAGCACTTTGGAG 1056
DB 2067 GAAAGCATCACTCAGGCGAGTGTGAGTGTACAGCTATGATCCAGCACTTTGGAG 2126
OY 1057 GCTGAGCGGGTGAATCACTGAGTGTAGAGTGTGAACACAGCTGGCCAACTGTGTA 1116
DB 2127 GCTGAGCGGGTGAATCACTGAGTGTAGAGTGTGAACACAGCTGGCCAACTGTGTA 2186

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OY 1117 AACCCATCTCTAATAAATACACAAATTAGCCGGGCGCTGGGGGGGCGCCACTTATGTC 1176
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Db 2187 AACCCATCTCTAATAAATACACAAATTAGCCGGGCGCTGGGGGGGCGCCACTTATGTC 2246
OY 1177 CCAGCTACTCAGAAAGCTGAGGCTGGGAAATGTTTGAACCCGGGAAAGCGAGTTGGAG 1236
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Db 2247 CCAGCTACTCAGAAAGCTGAGGCTGGGAAATGTTTGAACCCGGGAAAGCGAGTTGGAG 2306
OY 1237 GGAGCGGAGATACAGCCGATGACATCTCAGCCTGGGCGAGACAGCCAGAGTGTCTCAAA 1296
    |||||||
Db 2307 GGAGCGGAGATACAGCCGATGACATCTCAGCCTGGGCGAGAGAGAGTGTCTCAAA 2366
OY 1297 AGAAAAAAGAACCCGCTCCAAATGCTAATCTGCTTTTGTACATGGTGTAA 1356
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Db 2367 AGAAAAAAGAACCCGCTCCAAATGCTAATCTGCTTTTGTACATGGTGTAA 2426
OY 1357 AGTCAGATCCCAAGAGGCGCCAGGAGGCGCACATATTCAGTGTGGCTGGGCAAGA 1416
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Db 2427 AGTCAGATCCCAAGAGGCGCCAGGAGGCGCACATATTCAGTGTGGCTGGGCAAGA 2486
OY 1417 TAACGCACTTCTAAGTAATAATCTGCAATTTTAAAAAGTAGTACCACTCAGGCCA 1476
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Db 2487 TAACGCACTTCTAAGTAATAATCTGCAATTTTAAAAAGTAGTACCACTCAGGCCA 2546
OY 1477 ACAAGCCAGCAAGAAAGCCAACTCTGCAGGCGACATCCAAACCCGCACTGGCATTTGC 1536
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Db 2547 ACAAGCCAGCAAGAAAGCCAACTCTGCAGGCGACATCCAAACCCGCACTGGCATTTGC 2606
OY 1537 ACCCTCCGCTTCTACTCCGGGTGTGCTGACAGCCCGCGCTCTTCTGCTGTCTAGG 1596
    |||||||
Db 2607 ACCCTCCGCTTCTACTCCGGGTGTGCTGACAGCCCGCGCTCTTCTGCTGTCTAGG 2666
OY 1597 CCACACCATCTCTTCAGAGGAATTTTCAGAACTAGACATGACGAGTCCGTGAGCCAT 1656
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Db 2667 CCACACCATCTCTTCAGAGGAATTTTCAGAACTAGACATGACGAGTCCGTGAGCCAT 2726
OY 1657 CTCTCTACTCTCTACTCAGCCTAGACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTTC 1716
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Db 2727 CTCTCTACTCTCTACTCAGCCTAGACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTTC 2786
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Db 2787 CCCACTCCCACTCAATTCCTGGGCGCCCAAGAGGGGTGGCGCACTTGGTACATG 2846
OY 1777 GCCAGTGTGATCCCAAGTGGCCAGTGTGTCTGCTGTCTGTTGCGTGTGCGGTG 1836
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Db 2847 GCCAGTGTGATCCCAAGTGGCCAGTGTGTCTGCTGTCTGTTGCGTGTGCGGTG 2906
OY 1837 TGTAGCCCAAGGTGGTAAAGTGGCTGCTTGAAGCCAGACGCTGGGATTCCTC 1896
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Db 2907 TGTAGCCCAAGGTGGTAAAGTGGCTGCTTGAAGCCAGACGCTGGGATTCCTC 2966
OY 1897 CCCATTAGATCAGCTTCCCTCCCTCCAGGGCCAGGGCCCTGCAAGAGGGGAAACAGTGT 1956
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Db 2967 CCCATTAGATCAGCTTCCCTCCCTCCAGGGCCAGGGCCCTGCAAGAGGGGAAACAGTGT 3026
OY 1957 AGCCTGGCGCGGATTCCTGGGAGGAAGCAGTGTGAGGGCTCTCTGAAAAGCTCAGTCTCA 2016
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Db 3027 AGCCTGGCGCGGATTCCTGGGAGGAAGCAGTGTGAGGGCTCTCTGAAAAGCTCAGTCTCA 3086
OY 2017 GGACCATGGGATTAAGAGAGAGCATGAATTTGCTTAGCAGAGCAGGGCGAGGGTGATA 2076
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Db 3087 GGACCATGGGATTAAGAGAGAGCATGAATTTGCTTAGCAGAGCAGGGCGAGGGTGATA 3146
OY 2077 AATTGTGATTAATTCACCTGAGACTTGAGCTTGACAGTAACTATTGGAAGGGTGGAGA 2136
    |||||||
Db 3147 AATTGTGATTAATTCACCTGAGACTTGAGCTTGACAGTAACTATTGGAAGGGTGGAGA 3206
OY 2137 GCCCAGCATTTACATGAGAGCAAGAGGGTTTCCACCTCGAATTCAGATGTCACT 2196
    |||||||
Db 3207 GCCCAGCATTTACATGAGAGCAAGAGGGTTTCCACCTCGAATTCAGATGTCACT 3266
OY 2197 GCGTGGCTGAGTACGTCGACCTGTACTCAGAGGCTGAGGGAGGATCATCGAGCCC 2256

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Db 3267 GCGTGGCTGAGTACGATGACCTGACCTGTACTCAGAGAGGCTGAGGGAGGATCATCTGAGACCC 3326
OY 2267 AGGAGTTTGAGGGCTGACAGCCAGCATATGATGCGCCACTACACTGCAGCTGAGCAACAGA 2316
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Db 3327 AGGAGTTTGAGGGCTGACAGCCAGCATATGATGCGCCACTACACTGCAGCTGAGCAACAGA 3386
OY 2317 GTGAGACCTGTCTCTTAAGAAAAAAGTACAGATGCTGGGAGCTGGGACGTTCTG 2376
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Db 3387 GTGAGACCTGTCTCTTAAGAAAAAAGTACAGATGCTGGGAGCTGGGACGTTCTG 3446
OY 2377 CCCCATTTGACACCCACATGAGAGACATGATGAGCGCACCTGCCCTGTGGACAGCTCT 2436
    |||||||
Db 3447 CCCCATTTGACACCCACATGAGAGACATGATGAGCGCACCTGCCCTGTGGACAGCTCT 3506
OY 2437 GGGAGACCTCAGGCTTCCCTGGCATCAGAGGCGAGGCCGGGAAACGATGATTTGGAG 2496
    |||||||
Db 3507 GGGAGACCTCAGGCTTCCCTGGCATCAGAGGCGAGGCCGGGAAACGATGATTTGGAG 3566
OY 2497 ACTGTGTGGGCGCTTGGTTCCCTTGTGTGTGTGTGTGATCCCAAGCAATGAAGTTTG 2556
    |||||||
Db 3567 ACTGTGTGGGCGCTTGGTTCCCTTGTGTGTGTGTGTGATCCCAAGCAATGAAGTTTG 3626
OY 2557 CACTGTATGCTGAGACGGCATTTCTGCTTATCAATAAACCTGTTGTTTAAAAAAA 2613
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Db 3627 CACTGTATGCTGAGACGGCATTTCTGCTTATCAATAAACCTGTTGTTTAAAAAAA 3683

RESULT 5
ABK33466
ID ABK33466 standard; DNA: 3683 BP.
XX
AC ABK33466;
XX
DT 23-APR-2002 (first entry)
XX
DE Human TNF receptor II gene with SNP in exon 2.
XX
KW Human: anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW Chromosome 1p36; Infliximab therapy; Crohn's disease; malignant disorder;
KW Inflammatory disorder; chronic disease; receptor; gene;
KW Single nucleotide polymorphism; ds.
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OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 90..1475
FT FT /*tag= a
FT sig_peptide /product= "TNF receptor II variant #1"
FT FT /*tag= b
FT mat_peptide 150..1472
FT FT /*tag= c
FT FT replace (257, A)
FT FT /*tag= d
FT FT /standard_name= "Single nucleotide polymorphism"
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XX EPI172444 -A1.
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XX 16-JAN-2002.
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XX 10-JUL-2000; 2000BP-0114786.
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XX 10-JUL-2000; 2000BP-0114786.
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XX 10-JUL-2000; 2000BP-0114786.
XX
XX (CONA-) CONARIS RES INST GMBH.
XX
XX Schreiber S, Hampe J, Mascheretti S;
XX WPI; 2002-156651/21.
XX DR P-PSDB; AAU75173.
XX
XX Detecting non-responders to anti-human necrosis factor therapy.
XX

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PT comprises testing an individual for homozygosity for a single
PT nucleotide polymorphism in the gene coding for the tumour necrosis
PT factor receptor II

XX Claim 15: Page 29-33; 45pp; English.

XX The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC A/G) and one in exon 6 (position 587 T/G) which result in Lys586Asn
CC and Met169Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC infliximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC represents the human TNF receptor II gene containing the SNP in exon 2.

XX Sequence 3683 BP: 780 A; 1098 C; 1087 G; 718 T; 0 other:

Query Match 95.4% Score 2493; DB 24; Length 3683;
Best Local Similarity 99.4% Pred. No. 0;

Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY	97	GACCCCAACCCCATCTTGCTGCTAGACATTTCTCCCTGTGGCCATGGGACCCAGATC	156
Db	1167	GAGCCCGGGGGCCAGCCGGAGCTCAGATTCTTCCCTGGTGGCCATGGGACCCAGATC	1226
QY	157	AATGTACCTGTCATGTCGAAAGCTCTGTAGACAGCTTGACACAGCTCAGTCTCTCC	216
Db	1227	AATGTACCTGTCATGTCGAAAGCTCTGTAGACAGCTTGACACAGCTCAGTCTCTCC	1286
QY	217	CAACCCAGCTCCAAATGGGAGACAGATTTCCAGCCCTCGAGTCCCGGAGAGACAG	276
Db	1287	CAACCCAGCTCCAAATGGGAGACAGATTTCCAGCCCTCGAGTCCCGGAGAGACAG	1346
QY	277	CAGTCTCCCTTCTTCCAAAGGAGATGTCTTTCGATCAGCTGAGAGAGCCAGAGAC	336
Db	1347	CAGTCTCCCTTCTTCCAAAGGAGATGTCTTTCGATCAGCTGAGAGAGCCAGAGAC	1406
QY	337	CTGCTGGGAGACACCGAAGAGAGCCCTTCCCTTGGAGTGCCTGATGCTGGATGAAG	396
Db	1407	CTGCTGGGAGACACCGAAGAGAGCCCTTCCCTTGGAGTGCCTGATGCTGGATGAAG	1466
QY	397	CCAGTTAACAGAGCCGCTGTGGCTGTGTGTAAGCCAGGTGGGAGCCCTGGCAGG	456
Db	1467	CCAGTTAACAGAGCCGCTGTGGCTGTGTGTAAGCCAGGTGGGAGCCCTGGCAGG	1526
QY	457	ATGACCTGCGAAGGGGCGCTGCTTCCAGGCCCCCAGCACTAGAGCTTGAGGCTCT	516
Db	1527	ATGACCTGCGAAGGGGCGCTGCTTCCAGGCCCCCAGCACTAGAGCTTGAGGCTCT	1586
QY	517	TTTCGGGGCAAGTTCTCTAGTGGCCCTCCAGAGCCGACCTTCCCTCTAAGCTGAGGCC	576
Db	1587	TTTCGGGGCAAGTTCTCTAGTGGCCCTCCAGAGCCGACCTTCCCTCTAAGCTGAGGCC	1646
QY	577	AAGAGAGAGAGCGAGTGTGGGAAAGCTCTGCTGCCATGATGTTGCTCTCCGAGG	636
Db	1647	AAGAGAGAGAGCGAGTGTGGGAAAGCTCTGCTGCCATGATGTTGCTCTCCGAGG	1706
QY	637	GCTGGCTGGGATGAGAGCTTCCGGGGCATCTGGGCGCACTCCCTGACTCTGTGACCTG	696
Db	1707	GCTGGCTGGGATGAGAGCTTCCGGGGCATCTGGGCGCACTCCCTGACTCTGTGACCTG	1766
QY	697	CCCGGCCAGCTGACCTCCAGAGCTGGCTCTCGAGAGCCCTTGGGTTTGTGTTGTTG	756
Db	1767	CCCGGCCAGCTGACCTCCAGAGCTGGCTCTCGAGAGCCCTTGGGTTTGTGTTGTTG	1826
QY	757	TTTTGTTGTTGTTGTTGTTTCTCCCTGGGCTCTGCCAGCTCTGAGTTCCAGAAACCC	816
Db	1827	TTTTGTTGTTGTTGTTGTTTCTCCCTGGGCTCTGCCAGCTCTGAGTTCCAGAAACCC	1886

QY	817	CAGATCTCTTTCGAGAGAGGGGCTTTCGAGAGAGGAGGATGCTGCTGAGTCAACCAT	876
Db	1887	CAGATCTCTTTCGAGAGAGGGGCTTTCGAGAGAGGAGGATGCTGCTGAGTCAACCAT	1946
QY	877	GAAGACAGGACAGTCTGCTTCCAGAGCTGAGAGCTGCGGAGATGCTCTGGGCTCTGTG	936
Db	1947	GAAGACAGGACAGTCTGCTTCCAGAGCTGAGAGCTGCGGAGATGCTCTGGGCTCTGTG	2006
QY	937	TAGGAGAGAGTGGGAGCCCTGTAGGGAACGGGGTCTTCAAGTTAGCTCAGAGAGCTTG	996
Db	2007	TAGGAGAGAGTGGGAGCCCTGTAGGGAACGGGGTCTTCAAGTTAGCTCAGAGAGCTTG	2066
QY	997	GAAAGCATCACTCAGGCGAGGTGAGTGGCTCAGCCTATGATCCAGCACTTTGGGAG	1056
Db	2067	GAAAGCATCACTCAGGCGAGGTGAGTGGCTCAGCCTATGATCCAGCACTTTGGGAG	2126
QY	1057	GCTGAGGCGGGTGGATCAGCTGAGGTTAGAGCTTGAGACAGCAGCCTGGCCATGTGTA	1116
Db	2127	GCTGAGGCGGGTGGATCAGCTGAGGTTAGAGCTTGAGACAGCAGCCTGGCCATGTGTA	2186
QY	1117	AACCCATCTTACTAAATATAGAAATTTAGCCGGGCGTGGGCGGCACTATAGTC	1176
Db	2187	AACCCATCTTACTAAATATAGAAATTTAGCCGGGCGTGGGCGGCACTATAGTC	2246
QY	1177	CCAGCTACTCAGAGGCTGAGGCTGGGAATGTTTGAACCCGGGAGCGAGGTTGCAG	1236
Db	2247	CCAGCTACTCAGAGGCTGAGGCTGGGAATGTTTGAACCCGGGAGCGAGGTTGCAG	2306
QY	1237	GGAGCGAGATCAGCGCATGTCAGCTCCAGCCCTGGGCGAGACAGAGAGTCTGTCAA	1296
Db	2307	GGAGCGAGATCAGCGCATGTCAGCTCCAGCCCTGGGCGAGACAGAGAGTCTGTCAA	2366
QY	1297	AGAAAAAAGAGACACCGCTCCAAATGCTAACCTTCTCTTTGTGTCATGTTGTA	1356
Db	2367	AGAAAAAAGAGAGACCGCTCCAAATGCTAACCTTCTCTTTGTGTCATGTTGTA	2426
QY	1357	AGTCAGATCCCGAGAGGGGCCAGGCGACAGCCATATTCAGTGTGTGGCTGGGCAAGA	1416
Db	2427	AGTCAGATCCCGAGAGGGGCCAGGCGACAGCCATATTCAGTGTGTGGCTGGGCAAGA	2486
QY	1417	TACGCACTTCTAACAGAAATCTGCCAATTTTAAAAAGTAAGTACCACTAGGCCA	1476
Db	2487	TACGCACTTCTAACAGAAATCTGCCAATTTTAAAAAGTAAGTACCACTAGGCCA	2546
QY	1477	ACAAGCAAAGCAAAAGCCAACTCTGCCAGCAGCATCAACCCCGCACTGCAATTTGC	1536
Db	2547	ACAAGCAAAGCAAAAGCCAACTCTGCCAGCAGCATCAACCCCGCACTGCAATTTGC	2606
QY	1537	ACCTCGGCTTCACTCCGGGTGTGCTGCTGAGCCCGGCGCTCTTCTGCTGTCTAGG	1596
Db	2607	ACCTCGGCTTCACTCCGGGTGTGCTGCTGAGCCCGGCGCTCTTCTGCTGTCTAGG	2666
QY	1597	CCACACATCTCTCTTTCAGGGAATTTAGAACTAGAGATGAGTCCGTAAGCAT	1656
Db	2667	CCACACATCTCTCTTTCAGGGAATTTAGAACTAGAGATGAGTCCGTAAGCAT	2726
QY	1657	CTCTTACTTCTACTGAGCTTACAGACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTC	1716
Db	2727	CTCTTACTTCTACTGAGCTTACAGACCTCTCTCTCCCGAGAGGGGTGGTTCTCTTC	2786
QY	1717	CCCACTCCCACTTCAATTCCTGGGCGCCAAAGGGCTGGCCCTGCCACTTTGGTACATG	1776
Db	2787	CCCACTCCCACTTCAATTCCTGGGCGCCAAAGGGCTGGCCCTGCCACTTTGGTACATG	2846
QY	1777	GCAGTGTGATCCCAAGTGCAGTCTGTGTCTGCTGCTGTGCTGTGCTGTGGTGTG	1836
Db	2847	GCAGTGTGATCCCAAGTGCAGTCTGTGTCTGCTGCTGTGCTGTGCTGTGGTGTG	2906
QY	1837	TGTAGCCAAAGTGGTGAAGTTGAATGGCGCTTGAAGCCACTGAAGCTGGGATTCCTC	1896
Db	2907	TGTAGCCAAAGTGGTGAAGTTGAATGGCGCTTGAAGCCACTGAAGCTGGGATTCCTC	2966
QY	1897	CCCATTAGAGTCAAGCTTCCCTCCAGGGCCAGGGCCCTGCGAGAGGGGAACCACTGT	1956

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Db 2967 CCCATTAGAGTACAGCTTCCCTCCAGAGGCCAGGCGCTCCAGAGGGAAACCAAGTGT 3026
Oy 1957 ACCGTTGCCCCGATTTCTGGAGGAAGCAGGTTGAGGGCTCTCGAAAGGCTCACTCTCA 2016
Db 3027 AGCCTTGCCCGATTTCTGGAGGAAGCAGGTTGAGGGCTCTCGAAAGGCTCACTCTCA 3086
Oy 2017 GGAGCATGGGGATTAAGAGGAAGCATGMAATTGTCTAGACAGAGCAGGGGAGGTGATA 2076
Db 3087 GCAGCATGGGGATTAAGAGGAAGCATGMAATTGTCTAGACAGAGCAGGGGAGGTGATA 3146
Oy 2077 AATTGTGATTAATTCCACTGACCTTGACCTTGACCTGAACTATTGAGAGCGTGGAGA 2136
Db 3147 AATTGTGATTAATTCCACTGACCTTGAGCTTGAGCTGAACTATTGAGAGCGTGGAGA 3206
Oy 2137 GCCCAGCATTACCATGAGACAAAGAGGTTTCCACCCTGGAAATCAAGTGTGAGACT 2196
Db 3207 GCCCAGCATTACCATGAGACAAAGAGGTTTCCACCCTGGAAATCAAGTGTGAGACT 3266
Oy 2197 GCGTGGCTGCACTGACGTCACCTGTACTAGAGAGGCTGAGGGGAGATCACTGGAGCCC 2236
Db 3267 GCGTGGCTGCACTGACGTCACCTGTACTAGAGAGGCTGAGGGGAGATCACTGGAGCCC 3326
Oy 2257 AGGAGTTGAGGCTGACGAGGACTATGATGCGCCGCTACACTCAGCCTGAGCAACAGA 2316
Db 3327 AGGAGTTGAGGCTGACGAGGACTATGATGCGCCGCTACACTCAGCCTGAGCAACAGA 3386
Oy 2317 GTGAGACCCCTGTCTCTTAAGAAAAAAGTCAAGACTGCTGGAGACTGGCAGGTTTCTG 2376
Db 3387 GTGAGACCCCTGTCTCTTAAGAAAAAAGTCAAGACTGCTGGAGACTGGCAGGTTTCTG 3446
Oy 2377 CCCAATTGGAGCCCATGAGAGACATGATGAGAGGCACTGCCCCCTGGTGGACAGTCTT 2436
Db 3447 CCCAATTGGAGCCCATGAGAGACATGATGAGAGGCACTGCCCCCTGGTGGACAGTCTT 3506
Oy 2437 GGGAGAACCTGAGGCTTCTGGCATCACAGGAGAGCGGAGGAGGATGAAATTTGGAG 2496
Db 3507 GGGAGAACCTGAGGCTTCTGGCATCACAGGAGAGCGGAGGAGGATGAAATTTGGAG 3566
Oy 2497 ACTCTGTGGGGCTTGGTTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2556
Db 3567 ACTCTGTGGGGCTTGGTTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3626
Oy 2557 CACTGTATGCTGAGAGGCACTTCTATCAATAAACCTGTTTGTAAAAAAA 2613
Db 3627 CACTGTATGCTGAGAGGCACTTCTATCAATAAACCTGTTTGTAAAAAAA 3683

RESULT 6
ABK33467
ID ABK33467 standard; DNA: 3683 BP.
XX
AC ABK33467;
Df 23-APR-2002 (first entry)
XX
DE Human TNF receptor II gene with SNP in exon 6.
XX
KW Human; anti-tumour necrosis factor receptor II; TNF receptor II; SNP;
KW chromosome 1p36; infliximab therapy; Crohn's disease; malignant disorder;
KW inflammatory disorder; chronic disease; receptor; gene;
KW single nucleotide polymorphism; ds.
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OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 90..1475
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FT sig_peptide /*tag= b
FT mat_peptide 156..1472
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PN EPI172444-A1.
PD 16-JAN-2002.
PE 10-JUL-2000; 2000EP-0114786.
PR 10-JUL-2000; 2000EP-0114786.
PA (CONA-) CONARIS RES INST GMBH.
PI Schreiber S, Hampe J, Mascheretti S;
DR WPI: 2002-156651/21.
DR P-PSDB; AA075174.
XX
XX Claim 16; Page 35-39; 45pp; English.
PS
PS The present invention relates to a method for detecting non-responders
CC to anti-tumour necrosis factor (TNF) therapy. The method involves testing
CC an individual for homozygosity for at least one single nucleotide
CC polymorphism (SNP) in the gene coding for TNF receptor II, which is
CC located on chromosome 1p36. Two novel SNPs, one in exon 2 (position 168
CC A/G) and one in exon 6 (position 587 T/G) which result in Lys56Lys and
CC Met196Arg respectively, are also described. The method of the invention
CC is useful for detecting non-responders to anti-TNF therapy such as
CC infliximab therapy, or therapy of Crohn's disease. The genes containing
CC the 2 novel polymorphisms are useful for diagnostic purposes in
CC inflammatory, malignant or other chronic diseases. The present sequence
CC represents the human TNF receptor II gene containing the SNP in exon 6.
XX
SQ
Sequence 3683 BP: 780 A: 1098 C: 1088 G: 717 T: 0 other:
Query Match 95.4%: Score 2493; DB 24; Length 3683;
Best Local Similarity 99.4%: Pred. No. 0;
Matches 2502; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Oy 97 GACCCCCACCCCATTTGTGCTTAGCAGATCTTCCCTCCGTGGCCATGGAGCCAGGTC 156
Db 1167 GAGGCCCGGGCCAGACCCGGAGACTAGATCTTCCCTGGTGGCCATGGAGCCAGGTC 1226
Oy 157 AATGTCACCTGATCGTGAACGCTGTAGACAGCTGTGACACAGCTCAAGTGTCTTCC 216
Db 1227 AATGTCACCTGATCGTGAACGCTGTAGACAGCTGTGACACAGCTCAAGTGTCTTCC 1286
Oy 217 CAAGCAGCTCCACAATGGAGACACAGATTCCAGCCCTCGAGTCCCCGAAAGCAGAG 276
Db 1287 CAAGCAGCTCCACAATGGAGACACAGATTCCAGCCCTCGAGTCCCCGAAAGCAGAG 1346
Oy 277 CAGGTCCCTTCTCCAAAGAGGAATGTGCTTGGGTACAGCTGAGAGCCGAGAGACC 336
Db 1347 CAGGTCCCTTCTCCAAAGAGGAATGTGCTTGGGTACAGCTGAGAGCCGAGAGACC 1406
Oy 337 CTGCTGGGAGACCAAGAGAGCCCTGCCCCCTTGGAGTGGCTGATGCTGGATGAAG 396
Db 1407 CTGCTGGGAGACCAAGAGAGCCCTGCCCCCTTGGAGTGGCTGATGCTGGATGAAG 1466
Oy 397 CCCAGTTAACGAGGCGGGGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 456
Db 1467 CCCAGTTAACGAGGCGGGGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1526
Oy 457 ATGACCTGCGAAGGGGCGCTGTGCTTCCAGAGGCCCCACCACTAGAGACTGTGAGGCT 516
Db 1527 ATGACCTGCGAAGGGGCGCTGTGCTTCCAGAGGCCCCACCACTAGAGACTGTGAGGCT 1586
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Oy	517	TTCTGGGGCCAAAGTTTCCCTCTACGTGCCCCCTCACAGCCGCAAGCCTCCCTCTGACCTGCAGGCC	576
Db	1587	TTCTGGGGCCAAAGTTTCCCTCTACGTGCCCCCTCACAGCCGCAAGCCTCCCTCTGACCTGCAGGCC	1648
Oy	577	AAGAGCAGAGAGCGACGATGTTGGGGAAGCCCTCTGTCGCATGGGTGTCCCTCTGGGAAG	636
Db	1647	AAGAGCAGAGAGCGAGATGTTGGGGAAGCCCTCTGTCGCATGGGTGTCCCTCTGGGAAG	1706
Oy	637	GCTGGCTGGGCATGGACGTTCCGGGCCATGCTGGGGCAAGTCCCTGACCTCTGTGACCTG	696
Db	1707	GCTGGCTGGGCATGGACGTTCCGGGCCATGCTGGGGCAAGTCCCTGACCTCTGTGACCTG	1766
Oy	697	CCCCGCCACAGCTGCACCTGCCAGCCTGGCCTTCTGAGACCCCTTGGGGTTTTTGTGTTGGT	756
Db	1767	CCCCGCCACAGCTGCACCTGCCAGCCTGGCCTTCTGAGACCCCTTGGGGTTTTTGTGTTGGT	1826
Oy	757	TTTTGTTTGTGTTTGTGTTTCTTCCCTCGGCGCTGCGCCACCTGTGCCTTTCGAAAAACC	816
Db	1827	TTTTGTTTGTGTTTGTGTTTCTTCCCTCGGCGCTGCGCCACCTGTGCCTTTCGAAAAACC	1886
Oy	817	CAGCATCTCTTTCTGCAGAGGGGCTTCTGGAGAGGGAGATGCTGCTCGATCACCAT	876
Db	1887	CAGCATCTCTTTCTGCAGAGGGGCTTCTGGAGAGGGAGATGCTGCTCGATCACCAT	1946
Oy	877	GAAGACAGACAGTCTCTTACCTCTGAGCGTAGACTGCGGAGATGTCGCGGGCTCTGTG	936
Db	1947	GAAGACAGAGACAGTCTCTTACCTCTGAGCGTAGACTGCGGAGATGTCGCGGGCTCTGTG	2006
Oy	937	TAGGGAGAGGGGGGAGCGCCCTGTAGGGAAAGGGGGCTCTTCAAGTTAGCTCAGAGAGCTTG	996
Db	2007	TAGGGAGAGGGGGGAGCGCCCTGTAGGGAAAGGGGGCTCTTCAAGTTAGCTCAGAGAGCTTG	2066
Oy	997	GAAGACATCACCCTAGGCGAGGCTGACATGGCTCACCCCTATGATCCAGACATTGGGAG	1056
Db	2067	GAAGACATCACCCTAGGCGAGGCTGACATGGCTCACCCCTATGATCCAGACATTGGGAG	2126
Oy	1057	GCTGAGGGGGGTGGATCACCCTGAGAGTTAGAGTTTGCAGACACAGCCTGGCCAAATGTTAA	1116
Db	2127	GCTGAGGGGGGTGGATCACCCTGAGAGTTAGAGTTTGCAGACACAGCCTGGCCAAATGTTAA	2186
Oy	1117	AACCCCATCTCTACTAAAAAATACAGAAATTAGCCGGGCGCTGTGCGGGACCTATAGTC	1176
Db	2187	AACCCCATCTCTACTAAAAAATACAGAAATTAGCCGGGCGCTGTGCGGGACCTATAGTC	2246
Oy	1177	CCAGCTACTCAGAAAGCCTGAGGCTGGGAAATGCTTTGAACCCGGGAAAGGAGGTTGCAG	1236
Db	2247	CCAGCTACTCAGAAAGCCTGAGGCTGGGAAATGCTTTGAACCCGGGAAAGGAGGTTGCAG	2306
Oy	1237	GCAGCCGAGATCAGCGCAGTCAGCACTCAGCTGAGGGGAGCAGAGCGAGAGTGTCTCAA	1296
Db	2307	GCAGCCGAGATCAGCGCAGTCAGCACTCAGCTGAGGGGAGCAGAGCGAGTGTCTCAA	2366
Oy	1297	AGAAAAAAGAAAAAGCAGCCGCTCCAAATGCTAACTGTCTCTTTTGTACATGGTGTGAA	1356
Db	2367	AGAAAAAAGAAAAAGCAGCCGCTCCAAATGCTAACTGTCTCTTTTGTACATGGTGTGAA	2426
Oy	1357	AGTCAGATGGCCAGAGGGGCCAGGCGGCGACACATATTCAGTGTGTGGCTGGGCAAGA	1416
Db	2427	AGTCAGATGGCCAGAGGGGCCAGGCGGCGACACATATTCAGTGTGTGGCTGGGCAAGA	2486
Oy	1417	TAAAGCATCTTCTAATAGAAATCTGGCAATTTTTTAAAAAAGTAAGTACCACTCAGGCCA	1476
Db	2487	TAAAGCATCTTCTAATAGAAATCTGGCAATTTTTTAAAAAAGTAAGTACCACTCAGGCCA	2546
Oy	1477	ACAAGCCAAAGACAAAAAGCAAACTGTCCAGGCAATCAACACCCGCCACCTGCCATTTCG	1536
Db	2547	ACAAGCCAAAGACAAAAAGCAAACTGTCCAGGCAATCAACACCCGCCACCTGCCATTTCG	2606
Oy	1537	ACGCTCGGCTTCACTCGGCTGTGCTGCAGAGCCCGCGCTCTCTTCTGTCTGTCTAGG	1596
Db	2607	ACGCTCGGCTTCACTCGGCTGTGCTGCAGAGCCCGCGCTCTCTTCTGTCTGTCTAGG	2666
Oy	1597	CCACACATCTCTCTTCCAGGGAATTTCCAGAGAACTAGAGATGACGAGTCCCTGTAAGCAT	1656

D	b	2667	CCACACCATCTCCTTTCCAGAGAAATTTCAAGAACTAGAGAAATGACTGATCTCTGTAGCCAT	1718
O	y	1657	CTCTCTACTCTCTACCTCAACCTTAGACCCCTCCTCCTCCCCAGAGGGGTGGATTCTCTTC	1718
D	b	2727	CTCTCTACTCTCTACCTCAACCTTAGACCCCTCCTCCTCCTCCCCAGAGGGGTGGATTCTCTTC	2786
O	y	1717	CCCACTGCCACCTTCAATTCCTGGGGCCCCAAACGGGCTCCCTGCCACTTTGGTATATG	1776
D	b	2787	CCCACTGCCACCTTCAATTCCTGGGGCCCCAAACGGGCTCCCTGCCACTTTGGTATATG	2846
O	y	1777	GCCAGTGTGATCCCAAGTGTCTGTGCTGCCTGTGTGTGGCTGTGGTGGGTATG	1836
D	b	2847	GCCAGTGTGATCCCAAGTGTCTGTGCTGCCTGTGTGTGGCTGTGGTGGGTATG	2906
O	y	1837	TGTAGCCAGAGTGGGTAAAGTTGATGGCTGTGCTTGAAGCACTGAAGCTGGATTCTTC	1896
D	b	2907	TGTAGCCAGAGTGGGTAAAGTTGATGGCTGTGCTTGAAGCACTGAAGCTGGATTCTTC	2966
O	y	1897	CCCATTTAGAGTAGAGCTTTCCCTCCCAAGGGCCAGGGCCCTGTGAGGGGGAACACAGCT	1956
D	b	2967	CCCATTTAGAGTAGAGCTTTCCCTCCCAAGGGCCAGGGCCCTGTGAGGGGGAACACAGCT	3026
O	y	1957	AGCTTTGCCCGGATTTCTGGAGGAAGAGGTTGAGGGGCTCCTGTGAAAGGCTCAAGTCTCA	2016
D	b	3027	AGCTTTGCCCGGATTTCTGGAGGAAGAGGTTGAGGGGCTCCTGTGAAAGGCTCAAGTCTCA	3086
O	y	2017	GGAGCATGGGGGTAAAGGAGAAGGCATGAATTTGTCTACACAGCAGGGGCAAGGGTGATA	2076
D	b	3087	GGAGCATGGGGGTAAAGGAGAAGGCATGAATTTGTCTACACAGCAGGGGCAAGGGTGATA	3146
O	y	2077	AATTTGTGTAATTAATTCACAGTGTGAGCTTGGAGCTTGGAGCTTATTTGGAGGGTGGAGA	2136
D	b	3147	AATTTGTGTAATTAATTCACAGTGTGAGCTTGGAGCTTGGAGCTTATTTGGAGGGTGGAGA	3206
O	y	2137	GGCCAGCCCATTTACATGGAGACAAGAAGGGTTTTTCACCCTGGAAATCAAGATGTTCAGACT	2196
D	b	3207	GGCCAGCCCATTTACATGGAGACAAGAAGGGTTTTTCACCCTGGAAATCAAGATGTTCAGACT	3266
O	y	2197	GGCTGGCTGCAGTACAGTGCACCGTGTACTGAGAGGCTGAGGGAGATCTACTGGAAGCC	2256
D	b	3267	GGCTGGCTGCAGTACAGTGCACCGTGTACTGAGAGGCTGAGGGAGATCTACTGGAAGCC	3326
O	y	2257	AGGAGTTTGAAGCTGCAGCGAGGCTATGATCGGCGCACTAACATCCAGGCTGAGCAACAGA	2316
D	b	3327	AGGAGTTTGAAGCTGCAGCGAGGCTATGATCGGCGCACTAACATCCAGGCTGAGCAACAGA	3386
O	y	2317	GGGAGACCCCTCTCTTAAAGAAAAAAAGTGAAGTCTGTGGAGCTGGCCAGGTTTTCTG	2376
D	b	3387	GGGAGACCCCTCTCTTAAAGAAAAAAAGTGAAGTCTGTGGAGCTGGCCAGGTTTTCTG	3446
O	y	2377	CCCACTATGGACCCACATGTAGAGCATGATGAGAGCCACTTCCCTCGTGTGGACAGTCTCT	2436
D	b	3447	CCCACTATGGACCCACATGTAGAGCATGATGAGAGCCACTTCCCTCGTGTGGACAGTCTCT	3506
O	y	2437	GGGAGAACTTAGAGCTTCTTGGCATCACAGGGCAGAGCCGGGAAGGATGAATTTGGAG	2496
D	b	3507	GGGAGAACTTAGAGCTTCTTGGCATCACAGGGCAGAGCCGGGAAGGATGAATTTGGAG	3566
O	y	2497	ACTCTGTGGGGCCTTGGTTCCCTGTGTGTGTGTGTATATCCCAAGCAATGAAGTTTG	2556
D	b	3567	ACTCTGTGGGGCCTTGGTTCCCTGTGTGTGTGTGTATATCCCAAGCAATGAAGTTTG	3626
O	y	2557	CACGTATGCTGGAGCGGATTCCTCTTATCAATTAACCTTTGTTTAAAAAAA	2613
D	b	3627	CACGTATGCTGGAGCGGATTCCTCTTATCAATTAACCTTTGTTTAAAAAAA	3683

RESULT 7
AA010956
ID_---AA010956 standard; DNA; 2339 BP.
RX_

```
XX 24-MAY-1991 (first entry)
DT Encodes human 75kd TNF-binding protein.
XX
DE Tumour Necrosis Factor: binding proteins; septic shock;
XX autoimmune glomerulonephritis; lymphokine; cytokine.
XX
FH Key Location/Qualifiers
FT CDS 1..1179
FT /tag= a
FT /product= 75kd TNF-BP
FT
XX EPA17563-A.
XX
XX 20-MAR-1991.
XX
XX 31-AUG-1990: 90EP-0116707.
XX
XX 20-APR-1990: 90CH-0001347.
XX 12-SEP-1989: 89CH-0003319.
XX 08-MAR-1990: 90CH-0000746.
XX
XX (HOFF ) HOFFMANN-LA ROCHE AG.
XX
XX Brockhaus M, Demble Z, Gentz R, Lesslauer W, Lotscher H;
XX Schlieger EJ;
XX
XX WPI: 1991-081851/12.
XX P-PSDB: AAR11605.
XX
XX Insoluble tumour necrosis factor binding proteins - and DNA
XX encoding them, useful in pharmaceutical prods. and for antibody
XX prodn.
XX
XX Claim 4: Fig 1: 26pp; German.
XX
XX Partial amino acid sequences were determined for the 55 and 75kd
XX TNF-BPs (see AAR11072-R11081) and oligonucleotide primers were
XX synthesised based on these partial sequences. The primers were
XX used to produce a cDNA fragment for use as a probe to screen a human
XX placental cDNA bank constructed in lambda g11. Positive clones were
XX identified and sequenced. Repeated sequencing showed a discrepancy
XX at position 7 such that the third codon encodes either Thr or Ser.
XX cDNA constructs comprising the TNF-BP coding sequence may also
XX contain a fragment encoding a human Ig domain. Recombinant
XX constructs are used to transform cells to confer improved TNF-
XX binding properties.
XX See also AAQ10955.
XX
XX
XX Sequence 2339 BP; 494 A; 720 C; 685 G; 439 T; 1 other:
XX
Query Match 54.5%; Score 1423; DB 12; Length 2339;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 20; Indels 2; Gaps 2;
```

```
Db 1103 CAGAGACCCTGCGGAGCACCAGAAAGGCCCTGGCCCTTGAGAGTCCGATGCTG 1162
Oy 389 GGATGAGCCCGATTAAACACGCGGCTGTGGCTGTCTAGCAAGTGGCTAGCC 448
Db 1163 GGATTAACCCAGATTAAACAGGCGGTGTGGGCTGTCTAGCAAGT-6GCTAGCC 1221
Oy 449 CTGGCAGATGATCCCTGGGAAGGGGCCCTGTCTTCCAGAGCCCAACCACTAGACTCT 508
Db 1222 CTGGCAGATGATCCCTGGGAAGGGGCCCTGTCTTCCAGAGCCCAACCACTAGACTCT 1281
Oy 509 GAGGCTCTTTTGGGCCCAAGTCTCTAGTGCCCTCCAGACCGCAGCCCTCCCTGACC 568
Db 1282 GAGGCTCTTTTGGGCCCAAGTCTCTAGTGCCCTCCAGACCGCAGCCCTCCCTGACC 1341
Oy 569 TGCAGGCCAAGAGAGAGAGCGAGTGGGGAAGGCTCTGCTGCATGTGTGCTCCT 628
Db 1342 TGCAGGCCAAGAGAGAGAGCGAGTGGGGAAGGCTCTGCTGCATGTGTGCTCCT 1401
Oy 629 CTGCGAAGGCTGGCTGGCATGACGCTTCGGGCAATGCTGGGCAAGTCCCTGACTCT 688
Db 1402 CTCGGAAGGCTGGCTGGCATGACGCTTCGGGCAATGCTGGGCAAGTCCCTGACTCT 1461
Oy 689 GTGACCTGCCCCGCCGACCTGACCTGACCGCTGCTGAGCCCTTGGGCTTTTGG 748
Db 1462 GTGACCTGCCCCGCCGACCTGACCTGACCGCTGCTGAGCCCTTGGGCTTTTGG 1521
Oy 749 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 808
Db 1522 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1581
Oy 809 GAAACCCCGACATCCCTTTCTGACAGAGGCGCTTTTGAGAGAGAGATGCTGCTGAG 868
Db 1582 GAAACCCCGACATCCCTTTCTGACAGAGGCGCTTTTGAGAGAGAGATGCTGCTGAG 1641
Oy 869 TCACCATGAAGACAGACAGTGTCTGACCTGAGGCTGAGAGCTGGGATGCTGCTGG 928
Db 1642 TCACCATGAAGACAGAGAGTGTCTGACCTGAGGCTGAGAGCTGGGATGCTGCTGG 1701
Oy 929 GCTGTGTGAGGAGAGAGTGGGAGCCCTGTAGGAAAGGGGCTCTTAAAGTTAGCTAG 988
Db 1702 GCTGTGTGAGGAGAGAGTGGGAGCCCTGTAGGAAAGGGGCTCTTAAAGTTAGCTAG 1761
Oy 989 GAGGCTTGAAGACATCACTTACGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1048
Db 1762 GAGGCTTGAAGACATCACTTACGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1821
Oy 1049 TTTGGAGGCTGAGGCGGCTGATCACTGAGTTAGAGAGTTCAGAGACCACTGGCAA 1108
Db 1822 TTTGGAGGCTGAGGCGGCTGATCACTGAGTTAGAGAGTTCAGAGACCACTGGCAA 1881
Oy 1109 CATGATGAAGCCCATCTTACTATAAATAACAGAAATTAAGCCGGGCTGTGGCGGCAC 1168
Db 1882 CATGATGAAGCCCATCTTACTATAAATAACAGAAATTAAGCCGGGCTGTGGCGGCAC 1941
Oy 1169 CTATAGTCCAGTACTAGAAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1228
Db 1942 CTATAGTCCAGTACTAGAAAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2001
Oy 1229 GATTGAGGAGCCGAGATCAAGCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1288
Db 2002 GATTGAGGAGCCGAGATCAAGCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2061
Oy 1289 GTCTCAAAAGAAAAAAGCACCCTGCAAAATGCTAACTGTGTCCTTTTGTACCAT 1348
Db 2062 GTCTCAAAAG-AAAAAAGAAAAAGCACCCTGCAAAATGCTAACTGTGTCCTTTTGTACCAT 2120
Oy 1349 GGTGTGAAGTACATGCCAGAGGCGCCAGGACGAGCCACCATATTTCAGTGTGGCT 1408
Db 2121 GGTGTGAAGTACATGCCAGAGGCGCCAGGACGAGCCACCATATTTCAGTGTGGCT 2180
Oy 1409 GGGCAAGATAACGACTTCTACTAGTAATGTCATTTTAAAAAGTAAGTACAC 1468
```


Db 2181 GGGCAAGATACGCACTTCTACTAGAAATCTGCCATTTTAAAAAGTAGTACCAC 2240
QY 1469 TCAGGCCAACAGCCACAGACAAGTCAAACTCTGCAGCCACATCAACCCCCACCTG 1528
Db 2241 TCAGGCCAACAGCCACAGACAAGTCAAACTCTGCAGCCACATCAACCCCCACCTG 2300
QY 1529 CCATTGGACCCCTCCGCTTCACTCCGCTGCTGCTGCAAG 1567
Db 2301 CCATTGGACCCCTCCGCTTCACTCCGCTGCTGCTGCAAG 2339

RESULT 8

AAZ09171
ID AAZ09171 standard; cDNA: 2339 BP.

AC AAZ09171:

DT 18-OCT-1999 (first entry)

DE Human tumour necrosis factor binding protein cDNA fragment.

KM Tumour necrosis factor binding protein; TNF; insoluble protein; agonist;
KM anti-inflammatory; antimalarial; treatment; septic shock; inflammation;
KM autoimmune glomerulonephritis; cerebral malaria; immune response;
KM antagonist; diagnosis; ds.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 1..1179

FT /tag= a
FT /product= "TNF binding protein"
FT /note= "Partial sequence, no start codon given"

PN EP93121-A2.

PD 01-SEP-1999.

PF 31-AUG-1990; 90EP-0116707.

PR 20-APR-1990; 90CH-0001347.

PR 12-SEP-1989; 89CH-0003319.

PR 08-MAR-1990; 90CH-0000746.

PA (HOFF) HOFEMANN LA ROCHE & CO AG F.

PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Loetscher H;

DR WPI: 1999-480840/41.

DR P-PSDB: AAY30935.

PS Claim 4a: Fig 4: 25pp; German.

CC This invention describes novel homogeneous insoluble proteins (I),
CC their (in)soluble fragments (Ia) and their salts that can bind tumour
CC necrosis factor (TNF). The products of the invention have
CC anti-inflammatory and antimalarial activity. (i) and (Ia) are used (i)
CC to treat diseases in which TNF is involved (e.g. septic shock, autoimmune
CC glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
CC diagnostic determination of TNF in body fluids. Antibodies raised against
CC (i) are used for affinity purification of (i). This sequence encodes
CC a tumour necrosis factor binding protein fragment described in the method
CC of the invention.

XX Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;

Query Match 54.5%; Score 1423; DB 20; Length 2339;
Best Local Similarity 98.5%; Pred. No. 0.

Matches 1457; Conservative 0; Mismatches 20; Indels 2; Gaps 2;

QY 89 CCGGAGTACACCCCAACCCCAATCTTGTGTTAGCAGATTTCTCCCTGTGGCATGGGA 148
Db 863 CCGGAGAGGCGCGGGCCACACCGGAGCTCAGAGATTCTCCCTGTGGCATGGGA 922
QY 149 CCCAGGTCAATGTACACCTGCATGTGAACGTTCTGTAGACGCTTGACCAGCTACAGT 208
Db 923 CCCAGGTCAATGTACACCTGCATGTGAACGTTCTGTAGACGCTTGACCAGCTACAGT 982
QY 209 GCTCTCTCCCAAGCCACAGCTCCACAAATGGAGACACAGATTCCAGCCCTCGGAGTCCCGGA 268
Db 983 GCTCTCTCCCAAGCCACAGCTCCACAAATGGAGACACAGATTCCAGCCCTCGGAGTCCCGGA 1042
QY 269 AGGACGACGAGGTCCCTCTTCTCAAGAGAAATGTGCTTTCCGTTACAGCTGAGAGCG 328
Db 1043 AGGACGACGAGGTCCCTCTTCTCAAGAGAAATGTGCTTTCCGTTACAGCTGAGAGCG 1102
QY 329 CAGAGACCTCTGCGGAGACCCGAAGAGAGAGCCCTGCCCCCTTGAGTGCCTGATCTG 388
Db 1103 CAGAGACCTCTGCGGAGACCCGAAGAGAGAGCCCTGCCCCCTTGAGTGCCTGATCTG 1162
QY 389 GGATGAAGCCCAAGTTAACAGAGCCGCTGTGGCTGTGTCGTAAGCAAGTGGCGTGAAGC 448
Db 1163 GGATGAAGCCCAAGTTAACAGAGCCGCTGTGGCTGTGTCGTAAGCAAGT-GGCTGAAGC 1221
QY 449 CTGGCAGATGACCCCTGGGAGAGGCGCCCTGCTCTCCAGGCCCCACACTAGAGACTT 508
Db 1222 CTGGCAGATGACCCCTGGGAGAGGCGCCCTGCTCTCCAGGCCCCACACTAGAGACTT 1281
QY 509 GAGGCTCTTCTTGGGCGCAAGTTCCTAGTACCCCTCCACAGCCGACCCCTGCTGAC 568
Db 1282 GAGGCTCTTCTTGGGCGCAAGTTCCTAGTACCCCTCCACAGCCGACCCCTGCTGAC 1341
QY 569 TGCAGGCCCAAGAGCAGAGAGCAGCAGTTGGGAAAGCCCTGCTGCATGTTGCTCCCT 628
Db 1342 TGCAGGCCCAAGAGCAGAGAGCAGCAGTTGGGAAAGCCCTGCTGCATGTTGCTCCCT 1401
QY 629 CTCGGAAGGCTGCGTGGGCAATGAGAGGTTGGGGGATGCTGGGGCAAGTCCCTGACTCT 688
Db 1402 CTCGGAAGGCTGCGTGGGCAATGAGAGGTTGGGGGATGCTGGGGCAAGTCCCTGACTCT 1461
QY 689 GTGACCTGCCCCCGCCAGCTGACCTGACCTGCTTGTGAGGCTTGGGTTTGTG 748
Db 1462 GTGACCTGCCCCCGCCAGCTGACCTGACCTGCTTGTGAGGCTTGGGTTTGTG 1521
QY 749 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 808
Db 1522 TTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1581
QY 809 GAAACCCCAAGCATCTTTCTGACAGAGGGGCTTTGAGAGAGAGAGAGTGCCTGAG 868
Db 1582 GAAACCCCAAGCATCTTTCTGACAGAGGGGCTTTGAGAGAGAGAGAGTGCCTGAG 1641
QY 869 TCACCCATGAAGACAGACAGTCTTACGCTGAGCTGAGACTGGGAGTGTCTGTGG 928
Db 1642 TCACCCATGAAGACAGACAGTCTTACGCTGAGCTGAGACTGGGAGTGTCTGTGG 1701
QY 929 GCTCTGTGTAGGGAGAGGAGTGGAGCCCTGTAGGGAAGGGGCTCTTCAAGTTAGCTGAG 988
Db 1702 GCTCTGTGTAGGGAGAGGAGTGGAGCCCTGTAGGGAAGGGGCTCTTCAAGTTAGCTGAG 1761
QY 989 GAGGCTTGAAGACATCACCTCAGGCCAGGTGACAGTGGCTCAAGCTTATCCAGAC 1048
Db 1762 GAGGCTTGAAGACATCACCTCAGGCCAGGTGACAGTGGCTCAAGCTTATCCAGAC 1821
QY 1049 TTTGGGAGGCTGAGGGGGGTGATCAGCTGAGTTAGAGATTGAGACAGACTGGCCAA 1108
Db 1822 TTTGGGAGGCTGAGGGGGGTGATCAGCTGAGTTAGAGATTGAGACAGACTGGCCAA 1881
QY 1109 CATGTGTAACCCCATCTCTACTATAAAATACAGAAATTACGGGGGCTGTGGGGGAC 1168
Db 1882 CATGTGTAACCCCATCTCTACTATAAAATACAGAAATTACGGGGGCTGTGGGGGAC 1941

[illegible]


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QY 869 TCACCCATGACAGACGAGCAGTGTCTTACGCTGAGCTGAGACTGCGGATGTCCTGG 928
    |||||||
Db 1642 TCACCCATGACAGACGAGCAGTGTCTTACGCTGAGCTGAGACTGCGGATGTCCTGG 1701
    |||||||
QY 929 GCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 988
    |||||||
Db 1702 GCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1761
    |||||||
QY 989 GAGGCTTGGAAAGCATCTACCTCAGGCGGAGTGCAGTGCAGGCTTATGATGCCAGAC 1048
    |||||||
Db 1762 GAGGCTTGGAAAGCATCTACCTCAGGCGGAGTGCAGTGCAGGCTTATGATGCCAGAC 1821
    |||||||
QY 1049 TTTGGAGGCTGAGGCGGGGTGGATCCTGAGGTTTGGAGGTTTGGAGCCAGCTGGCCAA 1108
    |||||||
Db 1822 TTTGGAGGCTGAGGCGGGGTGGATCCTGAGGTTTGGAGGTTTGGAGCCAGCTGGCCAA 1881
    |||||||
QY 1109 CATGCTAAACCCCATCTCTCTAATAAATACAGAAATTAGCGGGGCGGTGGTGGGCGAC 1168
    |||||||
Db 1882 CATGCTAAACCCCATCTCTCTAATAAATACAGAAATTAGCGGGGCGGTGGTGGGCGAC 1941
    |||||||
QY 1169 CTATAGTCCCACTACTCAGAGGCTGAGGCTGGGAAATGTTTGAACCCGCGAAGCGGA 1228
    |||||||
Db 1942 CTATAGTCCCACTACTCAGAGGCTGAGGCTGGGAAATGTTTGAACCCGCGAAGCGGA 2001
    |||||||
QY 1229 GGTTCAGAGGAGCGGAGATCAGCGGCTGACACTGCAGCTGAGGCGAGACGAGAGTCT 1288
    |||||||
Db 2002 GGTTCAGAGGAGCGGAGATCAGCGGCTGACACTGCAGCTGAGGCGAGACGAGAGTCT 2061
    |||||||
QY 1289 GTCTCAAAAGAAAAAAGCAGCGCTCCAAATGATGATGTCCTTGTGTGTCAT 1348
    |||||||
Db 2062 GTCTCAAAAG-AAAAAAGCAGCGCTCCAAATGATGATGTCCTTGTGTGTCAT 2120
    |||||||
QY 1349 GGTGTGAAAGTCAAGATCCCAAGAGGCGCCAGAGGCGGACCATATTCAGTGTGGCCT 1408
    |||||||
Db 2121 GGTGTGAAAGTCAAGATCCCAAGAGGCGCCAGAGGCGGACCATATTCAGTGTGGCCT 2180
    |||||||
QY 1409 GGGCAGATATACGCACTTCTAAGTAAAGATCTGCAATTTTAAAGTAAGTACAC 1468
    |||||||
Db 2181 GGGCAGATATACGCACTTCTAAGTAAAGATCTGCAATTTTAAAGTAAGTACAC 2240
    |||||||
QY 1469 TCGAGGCCAAGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1528
    |||||||
Db 2241 TCGAGGCCAAGCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2300
    |||||||
QY 1529 CCATTTGACACCTTCGCGCTTCACTCCGCTGCTGCTGACAG 1567
    |||||||
Db 2301 CCATTTGACACCTTCGCGCTTCACTCCGCTGCTGCTGACAG 2339
    |||||||

RESULT 10
AAC83951
1D AAC83951 standard: DNA; 2394 BP.
XX
XX AAC83951:
XX
XX 02-MAR-2001 (first entry)
DE Human 40 kDa TNF inhibitor precursor coding sequence.
XX
XX TNF inhibitor: antiinflammatory; Tumour Necrosis Factor; interleukin;
KW IL-1; inflammatory disease; degenerative disease; human; lymphotoxin; ss.
XX
XX Homo sapiens.
XX
XX US6143866-A.
XX
XX 07-NOV-2000.
PD 19-JAN-1995; 95US-0375242.
PF 19-JUL-1990; 90US-0555274.
XX
XX 09-JUL-1993; 93US-0090366.
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PR 18-JUL-1989; 89US-0381080.
PR 11-DEC-1989; 89US-0450329.
PR 07-FEB-1990; 90US-0479661.
XX
XX (AMGE-) AMGEN INC.
PA Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI Vanderslice RW, Vannlice J, Kohno T;
DR WPI; 2001-006443/01.
XX
XX P-PSDB; AAB37686.
XX
XX Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT non-native cysteine residue cross-linked with polyethylene glycol,
PT useful for treating inflammatory and degenerative diseases mediated by
PT TNF.
XX
XX Example 12; Fig 39; 82pp: English.
XX
XX The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC novel TNF inhibitors of the present invention are useful as therapeutic
CC agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC for treating inflammatory and degenerative diseases mediated by TNF. The
CC present sequence is the coding sequence for the precursor of 40 kDa TNF
CC inhibitor. The 40 kDa TNF inhibitor can inhibit both TNF alpha and beta
CC (lymphotoxin).
XX
XX Sequence 2394 BP; 484 A; 743 C; 738 G; 428 T; 1 other;
SQ
Query Match 44.8%; Score 1171; DB 22; Length 2394;
Best Local Similarity 98.3%; Pred. No. 6.5e-303;
Matches 1194; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
QY 97 GACCCCAACCCCATCTTGTGCTTACAGATTTCTTCCCTGGTGGCATGGACCCAGGTC 156
    || ||| ||| |||
Db 1170 GAGGCCCGGGCCAGACCGGAGCTCAGATTCTTCCCTGGTGGCATGGACCCAGGTC 1229
    |||||||
QY 157 AATGTCACCTGATGTGTAACCTCTGTAGCAGCTGTGACACAGCTCAGCTGCTCTCC 216
    |||||||
Db 1230 AATGTCACCTGATGTGTAACCTCTGTAGCAGCTGTGACACAGCTCAGCTGCTCTCC 1289
    |||||||
QY 217 CAAGCCAGCTCCACATGAGGAGACACAGATTCAGAGCCCTCTGGAGTCCCGAAGAGAG 276
    |||||||
Db 1290 CAAGCCAGCTCCACATGAGGAGACACAGATTCAGAGCCCTCTGGAGTCCCGAAGAGAG 1349
    |||||||
QY 277 CAGGTCCTCTCTCCAGAGAGGAATGTGCTTGGTACAGCTGAGAGCCGACAGAGCC 336
    |||||||
Db 1350 CAGGTCCTCTCTCCAGAGAGGAATGTGCTTGGTACAGCTGAGAGCCGACAGAGCC 1409
    |||||||
QY 337 CTGCTGGGAGACACCGAAGAGAGAGCCCTGCTGAGTGCCTGAGTGCCTGAGTGAAG 396
    |||||||
Db 1410 CTGCTGGGAGACACCGAAGAGAGAGCCCTGCTGAGTGCCTGAGTGCCTGAGTGAAG 1469
    |||||||
QY 397 CCCAGTTAACCAAGCCGGGTGTGGGCTGTGCTGAGCCAAAGGTGGGCTGAGCCCTGGCAGG 456
    |||||||
Db 1470 CCCAGTTAACCAAGCCGGGTGTGGGCTGTGCTGAGCCAAAGGTGGGCTGAGCCCTGGCAGG 1529
    |||||||
QY 457 ATGACCCCTGGCAAGGGGCGCTGTGCTTCCAGAGCCGCCACCACTAGAGCTTGAAGCTCT 516
    |||||||
Db 1530 ATGACCCCTGGCAAGGGGCGCTGTGCTTCCAGAGCCGCCACCACTAGAGCTTGAAGCTCT 1589
    |||||||
QY 517 TTTCTGGGCAAGTTCTCTAGTGCCTCCACAGAGCGGAGGCTCCCTGTGACCTGACAGGC 576
    |||||||
Db 1590 TTTCTGGGCAAGTTCTCTAGTGCCTCCACAGGCGGAGGCTCCCTGTGACCTGACAGGC 1649
    |||||||
QY 577 AAGAGCAGAGGACGAGCTGGGAAAGCCTGTGCTTCCATAGTGTGTCCCTCTCGGAAG 636
    |||||||
Db 1650 AAGAGCAGAGGACGAGCTGGGAAAGCCTGTGCTTCCATAGTGTGTCCCTCTCGGAAG 1709
    |||||||
QY 637 GCTGGCTGGGCATGAGAGCTTCCGGGGCATGCTGGGCAAGTCCCTGACTCTGTGACGTC 696
    |||||||
Db 1710 GCTGGCTGGGCATGAGAGCTTCCGGGGCATGCTGGGCAAGTCCCTGACTCTGTGACGTC 1769
    |||||||
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Oy	697	CCCCGCCACGCTGCACCTCCAGCACCCTGGCTTTCGGAACCCCTTGATTTTGTGTTGTTG	756
Db	1770	CCCCGCCACGCTGCACCTCCAGCACCCTGGCTTTCGGAACCCCTTGATTTTGTGTTGTTG	1822
Oy	757	TTTTGTTGTTTGTGTTTGTTCGCCCGGGGCTCG-CCCAAGCTCTGGCTTCCAGAAACC	815
Db	1830	TTTTGTTGTTTGTGTTTGTTCGCCCGGGGCTCG-CCCAAGCTCTGGCTTCCAGAAACC	1883
Oy	816	CCAGCATCCTTTTCGACAGAGGGCTTTCTTGAGAGAGAGGAATCGCTCAATCACCCA	875
Db	1890	CCAGCATCCTTTTCGACAGAGGGCTTTCTTGAGAGAGAGGAATCGCTCAATCACCCA	1944
Oy	876	TCAAGACAGAGACAGTGTTCAGCCTGAGAGCTGAGACTGCGGGATGGTCTCGGGCTCTGT	935
Db	1950	TCAAGACAGAGACAGTGTTCAGCCTGAGAGCTGAGACTGCGGGATGGTCTCGGGCTCTGT	2005
Oy	936	GTAGGAGAGAGTGCGACGCCCTGTAGAGAAACGGGGTCTTCAATTAGCTCAGAGAGCTT	995
Db	2010	GCAGGAGAGAGTGCGACGCCCTGTAGAGAAACGGGGTCTTCAATTAGCTCAGAGAGCTT	2066
Oy	996	GGAAGACATTCACCTCAGGCCAGGTGCGAGTGGCTCAGCGCTATGATCCACGACCTTTGGGA	1055
Db	2070	GGAAGACATTCACCTCAGGCCAGGTGCGAGTGGCTCAGCGCTATGATCCACGACCTTTGGGA	2129
Oy	1056	GGCTGAGCGGGGTGGATCACCTGAGGTAGAGTTGAGACACAGCAGCCTGGCCAAATGGTA	1115
Db	2130	GGCTGAGCGGGGTGGATCACCTGAGGTAGAGTTGAGACACAGCAGCCTGGCCAAATGGTA	2188
Oy	1116	AACCCCATCTCTACTATAAATAATACAGAATAATACC CGGGCTGTGGCGGGCACCTATAGT	1179
Db	2190	AACCCCATCTCTACTATAAATAATACAGAATAATACC CGGGCTGTGGCGGGCACCTATAGT	2249
Oy	1176	CCCAGCTACTCAGAACGCTGAGAGCTGGGAANTGTTTGAACCCGGGAACCGAGAGTTTCA	1235
Db	2250	CCCAGCTACTCAGAACGCTGAGAGCTGGGAANTGTTTGAACCCGGGAACCGAGAGTTTCA	2309
Oy	1236	GGGAGCGAGATTCAGGCGACCTGCGACCTCCAGCCCTGGCGACAGACGAGAGTCTGTCAA	1295
Db	2310	GGGAGCGAGATTCAGGCGACCTGCGACCTCCAGCCCTGGCGACAGAGAGTCTGTCAA	2369
Oy	1296	AAGAAAAA AAAAAAAAA 1310	
Db	2370	AAGAAAAA AAAAAAAAA 2384	
RESULT 11			
ID	AAQ10907		
ID	AAQ10907	standard; cDNA: 2393 BP.	
XX	AAQ10907:		
AC	AAQ10907:		
XX	13-MAY-1991	(first entry)	
DT	40kD TNF inhibitor precursor gene in c40DK#6.		
XX	Tumour necrosis factor; Inhibitor; ss.		
KW	Homo sapiens.		
XX			
OS			
FH	Key	Location/Qualifiers	
FT	CDS	93..1478	
FT		/tag= a	
PF	16-JUL-1990:	90AU-0058976.	
PR	07-FEB-1990:	90US-0479661.	
PR	18-JUL-1989:	89US-0381080.	
R	11-DEC-1989:	89US-0450329.	

XX	(STINE-) SYNERGEN INC.
PA	WPI: 1991-073847/11.
DR	P-PSDB; AAR11001.
XX	Tumour necrosis factor inhibitor - for suppression of TNF-alpha
PT	and -beta, useful as therapeutic agent.
XX	Disclosure; Fig 39; 142pp; English.
XX	The sequence encodes the entire 40 kD TNF inhibitor. The clone from
CC	which the sequence was obld. was isolated from a cDNA library
CC	prep'd. from RNA form U937 cells treated with PMA/PHA. The whole
CC	gene can be inserted into expression vectors for prep'n. of TNF
CC	inhibitor for use in the treatment of inflammatory and degenerative
CC	diseases.
CC	See also AAQ10878, AAQ10884 and AAQ10883.
XX	
SQ	Sequence 2393 BP; 484 A; 743 C; 738 G; 428 T; 0 other;
	Query Match 64.4%; Score 1159; DB 12; Length 2193;
	Best Local Similarity 98.2%; Pred. No. 1.le-299;
	Matches 1193; Conservative 0; Mismatches 20; Indels 2; Gaps 2
OY	97 GACCCCACCCTATCTGTGCTTAGCAGATTCTTCCCTGGGGGCANTGGACCCAGTC 156
Db	1170 GAGCGCCGGGCCAGACACCGGAGACTCAGATTCTTCCCTGGTGCCATTGGACCCAGTTC 1229
OY	157 AATGTCACTCGCATCTGTGAACGCTGTGTAGCACACTGTGACACACAGCTCAGTGCCTCC 216
Db	1230 AATGTCACTCGCATCTGTGAACGCTGTGTAGCACACTGTGACACACAGCTCAGTGCCTCC 1289
OY	217 CAAGCCAGCTCCAAATGGGAGACACAGATTTCACAGCCCCCTGGAGTCCCGAAGGAGAG 276
Db	1290 CAAGCCAGCTCCAAATGGGAGACACAGATTTCACAGCCCCCTGGAGTCCCGAAGGAGAG 1349
OY	277 CAGTCCCTCTTCCCAAGAAGAAATGTGCTTTGGTACAGCTGTGAGACGCCAGAGACC 336
Db	1350 CAGTCCCTCTTCCCAAGAAGAAATGTGCTTTGGTACAGCTGTGAGAGGCCAGAGACC 1409
OY	337 CTGCTGGGGAGCACCGCAAGAGAGAGCCCTGGCCCTTGGAGTGCCTGATGTGGGATGAG 396
Db	1410 CTGCTGGGGAGCACCGCAAGAGAGAGCCCTGGCCCTTGGAGTGCCTGATGTGGGATGAG 1469
OY	397 CCAGATTAAACAGGCCGGCTGTGGGCTGTGTGTGTAGACCAGAGTGGGCTGAGCCCTGGCAG 456
Db	1470 CCAGATTAAACAGGCCGGCTGTGGGCTGTGTGTGTAGACCAGAGTGGGCTGAGCCCTGGCAG 1529
OY	457 ATGACCCCTCGAAGAGGGCCCTGTGCTTCCAGAGGCCCCACACATAGAGACATGAGGCTCT 516
Db	1530 ATGACCCCTCGAAGAGGGG-CCTGTGCTTCCAGAGGCCCCACACATAGAGACATGAGGCTCT 1588
OY	517 TTCTGGGCCCAAGTTCTCTAGTGGCCCTCACAGCCGACAGGCTCCCTGTGACTGCAGAGCC 576
Db	1589 TTCTGGGCCCAAGTTCTCTAGTGGCCCTCACAGCCGACAGGCTCCCTGTGACTGCAGAGCC 1648
OY	577 AAGAGCAGAGCAGCAGAGTGGGGAAAACCTCTGCTGCATGGTGTGTCCCTCTCGGAAG 636
Db	1649 AAGAGCAGAGCAGCAGAGGAGGTGTGGAAAAACCTCTGCTGCATGGTGTGTCCCTCTCGGAAG 1708
OY	637 GCCTGGCTGGGCATGSAAGTTGGGGCATGCTGGGGCAAGTCCCTGTGACTCTGTGACCTG 696
Db	1709 GCCTGGCTGGGCATGSAAGTTGGGGCATGCTGGGGCAAGTCCCTGTGACTCTGTGACCTG 1768
OY	697 CCCCGCCAGCTGCACCTGGCAGCCTGGCTTGTGGAGACCCCTTGGGTTTTTTGTTGTTTG 756
Db	1769 CCCCGCCAGCTGCACCTGGCAGCCTGGCTTGTGGAGACCCCTTGGGTTTTTTGTTGTTTG 1828
OY	757 TTGTGTTTGTGTTGTTGTCTTCCCTGGGCTGTG-CACAGCTGTGGCTTCAGAAAAACC 815
Db	1829 TTGTGTTTGTGTTGTTGTCTTCCCTGGGCTGTGCCCCCAGCTGTGGCTTCAGAAAAACC 1888

OY 816 CCAGCATCCCTTTCTGACAGAGGGGCTTTCTGAGAGAGAGGATGCTGCTGAGTACACCA 875
 DB 1889 CCAGCATCCCTTTCTGACAGAGGGGCTTTCTGAGAGAGAGGATGCTGCTGAGTACACCA 1948
 OY 876 TGAAGCAGACAGCTCTTCACTGAGGCTGAGACTGCGGATGCTGCTGGGCTCTGT 935
 DB 1949 TGAAGCAGACAGCTCTTCACTGAGGCTGAGACTGCGGATGCTGCTGGGCTCTGT 2008
 OY 936 GTAGGAGAGAGGCTGAGGCTCTGAGGAGAGGAGGCTCTTCAAGTTAGCTCAGAGGCTT 995
 DB 2009 GCAAGGAGAGGCTGAGGCTCTGAGGAGAGGAGGCTCTTCAAGTTAGCTCAGAGGCTT 2068
 OY 996 GGAAGCATCACCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 1055
 DB 2069 GGAAGCATCACCCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 2128
 OY 1056 GGCTGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 1115
 DB 2129 GGCTGAGGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 2188
 OY 1116 AACCCCATCTCTTAAATAATACAGAAATTAGCCGGGCTGAGGCTGAGGCTGAGGCTT 1175
 DB 2189 AACCCCATCTCTTAAATAATACAGAAATTAGCCGGGCTGAGGCTGAGGCTGAGGCTT 2248
 OY 1176 CCCACTACTGAGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 1235
 DB 2249 CCCACTACTGAGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 2308
 OY 1236 GGGAGCCGAGTCAAGCCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 1295
 DB 2309 GGGAGCCGAGTCAAGCCACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTT 2368
 OY 1296 AAGAAAAAATAA 1310
 DB 2369 AAGAAAAAATAA 2383

RESULT 12
 AA089544 standard; DNA: 2224 BP.
 AC AA089544;
 XX
 DT 31-OCT-1995 (first entry)
 XX
 DE p75 Tumour Necrosis Factor Receptor.
 XX
 KW Ligand; tumour necrosis factor; nerve growth factor; TNF; NGF;
 KM receptor; ss..
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 90..1475
 FT /tag= a
 FT /product= p75 TNF receptor.
 FT misc_difference 1137..1139
 FT /tag= b
 FT /transl_except= GCA encodes Glycine.
 FT misc_difference 1140..1142
 FT /tag= c
 FT /transl_except= CCA encodes Alanine.
 FT misc_difference 1146..1148
 FT /tag= d
 FT /transl_except= GTG encodes Glutamic acid.
 FT misc_difference 1149..1151
 FT /tag= e
 FT /transl_except= GAG encodes Alanine.
 FT misc_difference 1152..1154
 FT /tag= f
 FT /transl_except= GCC encodes Arginine.
 FT misc_difference 1155..1157
 FT /tag= g
 FT /tag= 9

FT /transl_except= AGT encodes Alanine.
 FT misc_difference 1158..1160
 FT /tag= h
 FT /transl_except= GCG encodes Serine.
 FT misc_difference 1161..1163
 FT /tag= i
 FT /transl_except= GCC encodes Threonine.
 FT misc_difference 1167..1169
 FT /tag= j
 FT /transl_except= GAG encodes Serine.
 FT misc_difference 1170..1172
 FT /tag= k
 FT /transl_except= GCC encodes Serine.
 FT misc_difference 1173..1175
 FT /tag= l
 FT /transl_except= CGG encodes Aspartic acid.
 FT misc_difference 1176..1178
 FT /tag= m
 FT /transl_except= GCC encodes Serine.
 FT misc_difference 1182..1184
 FT /tag= n
 FT /transl_except= ACC encodes Proline.
 FT misc_difference 1188..1190
 FT /tag= o
 FT /transl_except= ACC encodes Glycine.
 FT misc_difference 1191..1193
 FT /tag= p
 FT /transl_except= TCA encodes Histidine.
 FT misc_difference 1194..1196
 FT /tag= q
 FT /transl_except= GAT encodes Glycine.
 FT misc_difference 1197..1199
 FT /tag= r
 FT /transl_except= TCT encodes Threonine.
 FT misc_difference 2000..2002
 FT /tag= s
 FT /transl_except= TCC encodes Glutamine.
 FT misc_difference 2003..2005
 FT /tag= t
 FT /transl_except= CCT encodes Alanine.
 FT misc_difference 2006..2008
 FT /tag= u
 FT /transl_except= GGT encodes Proline.
 FT misc_difference 2012..2014
 FT /tag= v
 FT /transl_except= CAT encodes Valine.
 FT misc_difference 2015..2016
 FT /tag= w
 FT /transl_except= GCG encodes Glutamic acid.
 FT misc_difference 2017..2018
 FT /tag= x
 FT /transl_except= ACC encodes Alanine.
 FT misc_difference 2019..2021
 FT /tag= y
 FT /transl_except= CAG encodes Serine.
 PN EP648783-A.
 XX
 PD 19-APR-1995.
 XX
 PF 11-OCT-1994; 94EP-0116015.
 XX
 PR 12-OCT-1993; 93IL-0107267.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 PA (WALL/) WALLACH D.
 XX
 PI Beletsky I, Bigda J, Mett I, Wallach D;
 XX
 DR WPI: 1995-148673/20.
 DR P-PSDB: AAR72504.
 XX
 PT Tumour necrosis factor (TNF) receptor ligand - used to increase

PT Inhibitory effect of a soluble TNF receptor
 XX
 PS Disclosures: Figure 2; 18pp; English.

CC A ligand to a member of the tumour necrosis factor (TNF)/nerve
 CC growth factor (NGF) receptor family which binds either to the region
 CC of the 4th-Cys rich domain of the receptor, or to the region between
 CC it and the cell membrane may be used in the production of a
 CC pharmaceutical composition for increasing the inhibitory effect of a
 CC soluble receptor of the TNF/NGF receptor family. This sequence
 CC encodes the p75 TNF receptor. N in the sequence represents an
 CC unidentified nucleotide (poor reproduction in specification).
 XX

SO Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other:

Query Match 39.1%; Score 1022.8; DB 16; Length 2224;
 Best Local Similarity 97.9%; Pred. No. 2,9e-263;

Matches 1036; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 97 GACCCCAACCCATCTTGTGCTTACAGATTTCTCCCTGTGCTGACCCAGATC 156
 DB 1167 GAGGCGGCGGACGACCGGAGAGCTGATTTCTCCCTGTGCTGACCCAGATC 1226
 QY 157 AATGTACCTGATGATGAACTGTGTAGACCTGTGACACAGCTCAGATGCTCTCC 216
 DB 1227 AATGTACCTGATGATGAACTGTGTAGACCTGTGACACAGCTCAGATGCTCTCC 1286
 QY 217 CAAGCCAGCTCCACAATGAGAGACACAGATTCACAGCCCTGAGATCCCGAAGAGCAG 276
 DB 1287 CAAGCCAGCTCCACAATGAGAGACACAGATTCACAGCCCTGAGATCCCGAAGAGCAG 1346
 QY 277 CAGGTCCCTTCTCCAGAGAGAAATGCTGCTTGGGTACAGCTGAGAGCCAGAGACC 336
 DB 1347 CAGGTCCCTTCTCCAGAGAGAAATGCTGCTTGGGTACAGCTGAGAGCCAGAGACC 1406
 QY 337 CTGCTGGGAGACACCGAAGAGAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
 DB 1407 CTGCTGGGAGACACCGAAGAGAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1466
 QY 397 CCGAGTTACAGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 456
 DB 1467 CCGAGTTACAGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1526
 QY 457 ATGACCTGCGAGAGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 516
 DB 1527 ATGACCTGCGAGAGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1586
 QY 517 TTTCTGGGCGAAGTCTCTTGTAGTGCCTTCACAGCCGAGCCTCTCTGACCTGACGCC 576
 DB 1587 TTTCTGGGCGAAGTCTCTTGTAGTGCCTTCACAGCCGAGCCTCTCTGACCTGACGCC 1646
 QY 577 AAGAGCAGAGCAGCAGATTTGGGAAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636
 DB 1647 AAGAGCAGAGCAGCAGATTTGGGAAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1706
 QY 637 GCTGCTGGGCGATGAGAGCTTGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696
 DB 1707 GCTGCTGGGCGATGAGAGCTTGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1766
 QY 697 CCGCGCCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 756
 DB 1767 CCGCGCCAGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1826
 QY 757 TTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 816
 DB 1827 TTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1886
 QY 817 CAGCATCTTTTCTGCAAGAGGGGCTTCTGCAAGAGGAGGATGCTGCTGATCACCCT 876
 DB 1887 CAGCATCTTTTCTGCAAGAGGGGCTTCTGCAAGAGGAGGATGCTGCTGATCACCCT 1946
 QY 877 GAAGACAGCAGCTGCTTACAGCTGAGGCTGAGCTGCGGAGTGGTCTGCGGCTCTGTG 936
 DB 877 GAAGACAGCAGCTGCTTACAGCTGAGGCTGAGCTGCGGAGTGGTCTGCGGCTCTGTG 936

DB 1947 GAAGACAGCAGCTGCTTACAGCTGAGGCTGAGACTGCGGAGTGGTCTGCGGCTCTGTG 2006
 QY 937 TAGGAGAGAGTGTGACGCCCTGTAGGAGAAAGGGGCTTCAAGTTAGCTGAGAGGCTTG 996
 DB 2007 TAGGAGAGAGGCGGACGCCCTGTAGGAGAAAGGGGCTTCAAGTTAGCTGAGAGGCTTG 2066
 QY 997 GAAGCATCTCTACAGCCAGGCTGAGTGGCTTCACAGCCTATGATCCAGCACTTGGGAG 1056
 DB 2067 GAAGCATCTCTACAGCCAGGCTGAGTGGCTTCACAGCCTATGATCCAGCACTTGGGAG 2126
 QY 1057 GCTGAGCGGCGGTGATCACTGAGCTTGTAGAGCTTGTGAGACAGCTGCTGCAACATGCTAA 1116
 DB 2127 GCTGAGCGGCGGTGATCACTGAGCTTGTAGAGCTTGTGAGACAGCTGCTGCAACATGCTAA 2186
 QY 1117 AACCCCATCTCTACTAAATAACAAATAATAGCCGGGC 1154
 DB 2187 AACCCCATCTCTACTAAATAATAGCAATAATAGCCGGGC 2224

RESULT 13

ABK83541/C
 ID ABK83541 standard; cDNA; 733 BP.

XX ABK83541;

DT 14-AUG-2002 (first entry)

DE Human cDNA differentially expressed in granulocytic cells #112.

XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KM viral infection; parasitic infection; protozoal infection;
 KM fungal infection; sterile inflammatory disease; psoriasis;
 KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KM cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KM adult respiratory distress syndrome; inflammatory bowel disease;
 KM Crohn's disease; ulcerative colitis; peridontal disease;
 KM granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

OS MO200228999-A2.

PN 11-APR-2002.

PD 03-OCT-2001; 2001MO-US30821.

PE 03-OCT-2000; 2000US-237189P.

PR (GENE-) GENE LOGIC INC.

PA Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX MPI; 2002-435328/46.

DR Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity

XX Claim 1: SEQ ID No 112; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially)
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a

CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
 CC particularly in conditions in which both TNF and IL-1 play a causative
 CC role. They may be used to treat cachexia, rheumatoid arthritis,
 CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
 CC cerebral malaria, allograft and xenograft rejection in graft verses
 CC host disease, sepsis, septic shock, inflammation, allergies and
 CC autoimmune dysfunctions.

SQ Sequence 1641 BP; 328 A; 544 C; 502 G; 267 T; 0 other:

Query Match 17.3%: Score 453; DB 14; Length 1641;

Best Local Similarity 96.9%: Pred. No. 8.1e-111;

Matches 462; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 97 GACCCACCACCTCTTGTCTTACGATTTCTCCCTGTGTGCGCATGGAGCCAGGTC 156
 DB 1165 GAGGCCGGGGCCAGCACCAGGAGCTCAGATTTCTCCCTGTGTGCGCATGGAGCCAGGTC 1224
 OY 157 AATGTACCTGATGCTGAACGCTGTACAGCTGTGACACAGCTCAGAGTCTCTCC 216
 DB 1225 AATGTACCTGATGCTGAACGCTGTGTAGACCTGTGACACAGCTCAGAGTCTCTCC 1284
 OY 217 CAAGCCAGCTCCACAAATGGAGACAGATTCCAGCCCTCGAGATCCCGAAGAGCAG 276
 DB 1285 CAAGCCAGCTCCACAAATGGAGACAGATTCCAGCCCTCGAGATCCCGAAGAGCAG 1344
 OY 277 CAGGTCCCTTCTCCAGAGAGAAATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 336
 DB 1345 CAGGTCCCTTCTCCAGAGAGAAATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 1404
 OY 337 CTCTGCGGAGACACCAAGAGAGCCCTGCGCTTGGAGTCCCGATGCTGGATGAG 396
 DB 1405 CTGCTGGGAGACACCAAGAGAGCCCTGCGCTTGGAGTCCCGATGCTGGATGAG 1464
 OY 397 CCCAGTTAACCAAGCGCGGTGTGTGCTGTAGCCCAAGTGGGCTGAGCCCTGGCAG 456
 DB 1465 CCCAGTTAACCAAGCGCGGTGTGTGCTGTAGCCCAAGTGGGCTGAGCCCTGGCAG 1524
 OY 457 ATGACCCCTCGAAGGCGCGCTGTCTTCAGGCGCCCAACACTAGAGACTGTAGGCTCT 516
 DB 1525 ATGACCCCTCGAAGGCGCGCTGTCTTCAGGCGCCCAACACTAGAGACTGTAGGCTCT 1584
 OY 517 TTCTGGGCGCAAGTCTCTAGTGCCTTCAGAGCGGAGCCCTGCTGAGACTCTCAG 573
 DB 1585 TTCTGGGCGCAAGTCTCTAGTGCCTTCAGAGCGGAGCCCTGCTGAGACTCTCAG 1641

RESULT 15

AA045224
 ID AA045224 standard; cDNA: 1641 BP.

AC AA045224:

DT 07-OCT-1994 (first entry)

DE Sequence encoding human tumour necrosis factor receptor type I
 DE (TNFR1).

KW Tumour necrosis factor receptor; type I; TNFR1: arthritis therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT mat_peptide 154..1470

FT sig_peptide 88..153

FT /*tag= a

FT /*tag= b

XX MO9406476-A.

XX 31-MAR-1994.

XX 14-SEP-1993; 93MO-US08666.

XX 15-SEP-1992; 92US-0946236.

XX (IMMUNEX CORP.

XX Jacobs CA, Smith CA;

XX P-PSDB: AAR51002.

XX WPI: 1994-118172/14.

XX DR P-PSDB: AAR51002.

XX PT esp. soluble form of TNF receptor, opt. as fusion protein with

XX human immunoglobulin Fc region, esp. for treating arthritis

XX PT esp. soluble form of TNF receptor, opt. as fusion protein with

XX human immunoglobulin Fc region, esp. for treating arthritis

XX Disclosure: Page 28-30; 47pp; English.

AA045224 is cDNA from clone 1 of library WI-26 VA4 of human fibroblast
 cell 1 line WI-26 VA4. The mature full-length TNFR1 is a glycoprotein
 having a mol. wt. of about 75-80 kDa. The cloning of the cDNA for
 CC TNFR1 was described in Smith et al., Science 248:1019,1990. Clone 1
 CC is contained in expression vector pCAV/Not-TNFR (ATCC 68088). The
 CC and TNFR1 having at least 20 AAs. Soluble TNFR constructs are
 CC devoid of a transmembrane region but retain the ability to bind TNF.
 CC Examples of soluble TNFRs are hTNFR1delta235, hTNFR1delta165 and
 CC hTNFR1delta163 which encode respectively AAs 1-235, 1-185 and 1-163
 CC of AAR51002. An equivalent soluble TNFR is hTNFR1delta163 wherein x
 CC is selected from any one of AAs 163-235 of AAR51002.

SQ Sequence 1641 BP; 328 A; 526 C; 520 G; 267 T; 0 other:

Query Match 17.3%: Score 453; DB 15; Length 1641;

Best Local Similarity 96.9%: Pred. No. 8.1e-111;

Matches 462; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 97 GACCCACCACCTCTTGTCTTACGATTTCTCCCTGTGTGCGCATGGAGCCAGGTC 156
 DB 1165 GAGGCCGGGGCCAGCACCAGGAGCTCAGATTTCTCCCTGTGTGCGCATGGAGCCAGGTC 1224
 OY 157 AATGTACCTGATGCTGAACGCTGTACAGCTGTGACACAGCTCAGAGTCTCTCC 216
 DB 1225 AATGTACCTGATGCTGAACGCTGTGTAGACCTGTGACACAGCTCAGAGTCTCTCC 1284
 OY 217 CAAGCCAGCTCCACAAATGGAGACAGATTCCAGCCCTCGAGATCCCGAAGAGCAG 276
 DB 1285 CAAGCCAGCTCCACAAATGGAGACAGATTCCAGCCCTCGAGATCCCGAAGAGCAG 1344
 OY 277 CAGGTCCCTTCTCCAGAGAGAAATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 336
 DB 1345 CAGGTCCCTTCTCCAGAGAGAAATGTGCTTGTGCTACAGCTGTGAGAGCCAGAGAC 1404
 OY 337 CTGCTGGGAGACACCAAGAGAGCCCTGCGCTTGGAGTCCCGATGCTGGATGAG 396
 DB 1405 CTGCTGGGAGACACCAAGAGAGCCCTGCGCTTGGAGTCCCGATGCTGGATGAG 1464
 OY 397 CCCAGTTAACCAAGCGCGGTGTGTGCTGTAGCCCAAGTGGGCTGAGCCCTGGCAG 456
 DB 1465 CCCAGTTAACCAAGCGCGGTGTGTGCTGTAGCCCAAGTGGGCTGAGCCCTGGCAG 1524
 OY 457 ATGACCCCTCGAAGGCGCGCTGTCTTCAGGCGCCCAACACTAGAGACTGTAGGCTCT 516
 DB 1525 ATGACCCCTCGAAGGCGCGCTGTCTTCAGGCGCCCAACACTAGAGACTGTAGGCTCT 1584
 OY 517 TTCTGGGCGCAAGTCTCTAGTGCCTTCAGAGCGGAGCCCTGCTGAGACTCTCAG 573
 DB 1585 TTCTGGGCGCAAGTCTCTAGTGCCTTCAGAGCGGAGCCCTGCTGAGACTCTCAG 1641

Search completed: December 5, 2002, 23:29:22
 Job time : 723.284 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:39:29 ; Search time 5001.06 Seconds

(Without alignments)
8461.969 Million cell updates/sec

Title: US-09-856-937a-1
Perfect score: 2613
Sequence: 1 tctgtctcgcgtcctgcgc.....ccctgttctttaaaaaa 2613

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpi:*
7: em_estro:*
8: em_hlc:*
9: gq_estl:*
10: gq_estl2:*
11: gq_hlc:*
12: gq_estl3:*
13: gq_estl4:*
14: gq_estl5:*
15: em_estlun:*
16: em_estlom:*
17: gq_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174.2	44.9	2291	11	BC011844 Homo sapi
2	864.2	33.1	1029	14	BQ053081 AGENCOURT
3	839.8	33.1	1075	14	BQ052380 AGENCOURT
4	811	31.0	1022	14	BM914358 AGENCOURT
5	810.8	31.0	1053	14	BQ052282 AGENCOURT
6	797.2	30.5	945	14	BQ690571 AGENCOURT

7	745.4	28.5	771	13	BI838021	BI838021 603083869
8	696.2	26.6	1183	12	BF569011	BF569011 602184353
9	684.6	26.2	752	12	AT762184	AT762184 w90h12.x
10	682.6	26.1	697	9	AT935824	AT935824 w05c01.x
11	675	25.8	759	13	BI911067	BI911067 603069712
12	650.6	24.9	958	12	BC746069	BC746069 602723532
13	629.8	24.1	655	14	BO632819	BO632819 1128d03.y
14	624.6	23.9	672	10	BE440065	BE440065 HTM1-1841
15	613.2	23.5	733	9	AT813532	AT813532 w183a09.x
16	610.6	23.4	656	13	BT161001	BT161001 602865207
17	608.6	23.3	932	12	BC829828	BC829828 602764119
18	574	22.0	633	10	BM794931	BM794931 K-EST0076
19	567.6	21.7	630	14	BE299702	BE299702 600944393
20	562.8	21.5	1068	14	BO706144	BO706144 AGENCOURT
21	560	21.4	570	14	BM993941	BM993941 UT-H-DT0-
22	550.8	21.1	566	14	BO632532	BO632532 1128d03.x
23	550	21.0	550	9	AT880380	AT880380 at47h02.x
24	547.6	21.0	1470	12	BF569050	BF569050 602184408
25	545.8	20.9	1102	14	BM917316	BM917316 AGENCOURT
26	540.8	20.7	572	14	BM678005	BM678005 UT-E-EJ0-
27	534	20.4	534	10	AM170706	AM170706 x196a06.x
28	528.4	20.2	542	14	BM725892	BM725892 UT-E-EJ0-
29	526.2	20.1	1066	12	BF568708	BF568708 602184353
30	525.8	20.1	760	13	BI161017	BI161017 602865227
31	522.6	20.0	1051	12	BF568409	BF568409 602184408
32	501.4	19.2	516	10	BE042561	BE042561 h025f06.x
33	490	18.8	499	14	BM769522	BM769522 K-EST0052
34	487.4	18.7	489	9	AU185817	AU185817 AU185817
35	470	18.0	470	10	BE138861	BE138861 xx96f07.x
36	469.6	18.0	562	14	W03113	W03113 za53a04.r1
37	462	17.7	462	10	BE042997	BE042997 h031f01.x
38	454	17.4	454	9	AM468069	AM468069 h031e06.x
39	453.4	17.4	460	10	AM468069	AM468069 h031e06.x
40	448.4	17.2	454	9	AT422018	AT422018 tf45901.x
41	446	17.1	446	9	AT140025	AT140025 q968909.x
42	440	16.8	440	9	AA972749	AA972749 q901e03.s
43	437.4	16.7	452	9	AA934488	AA934488 O050b05.s
44	425.8	16.3	429	9	AT693889	AT693889 w064g01.x
45	425	16.3	513	9	AT434325	AT434325 t141d04.x

ALIGNMENTS

RESULT 1
LOCUS BC011844 2291 bp mRNA linear HTC 02-AUG-2001
DEFINITION Homo sapiens, Similar to tumor necrosis factor receptor superfamily, member 1B, clone IMAGE:4111730, mRNA.
ACCESSION BC011844
VERSION BC011844.1 GI:15080140
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2291)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>

REMARK COMMENT


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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="534648"
/clone_lib="NIH_MGC_106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: blood; Vector: pORF7; Site: 1; XhoI: Site 2; EcoRI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGACGAC(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT      227 a      306 c      277 g      210 t      9 others
ORIGIN

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Query Match      33.1% Score 864.2; DB 14; Length 1029;
Best Local Similarity 97.8%; Pred. No. 1,1e-130;
Matches 905; Conservative 0; Mismatches 17; Indels 3; Gaps 3:

QY 1477 ACAAGCCAAAGCAAGCAAACTGCGAGCCATCCAAACCCCACTGCTGCTAGG 1536
    |
DB 1 ACAAGCCAAAGCAAGCAAACTGCGAGCCATCCAAACCCCACTGCTGCTAGG 60

QY 1537 ACCCTCCGCTTCACTCCGCTGCTGCTGCAAGCCCGGCTCTGCTGCTGCTAGG 1596
    |
DB 61 ACCCTCCGCTTCACTCCGCTGCTGCTGCAAGCCCGGCTCTGCTGCTGCTAGG 120

QY 1597 CCACACCATCTCTTTTCAAGGAATTTTCAAGACTAGATGATGATGATGATGATGAT 1656
    |
DB 121 CCACACCATCTCTTTTCAAGGAATTTTCAAGACTAGATGATGATGATGATGATGAT 180

QY 1557 CTCTCTACTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1716
    |
DB 181 CTCTCTACTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

QY 1717 CCCACTCCCACTTCAATTTCTGCGGCCCAAGGGGCTGCTGCTGCTGCTGCTGCTG 1776
    |
DB 241 CCCACTCCCACTTCAATTTCTGCGGCCCAAGGGGCTGCTGCTGCTGCTGCTGCTG 300

QY 1777 GCCAGTGTGATGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1836
    |
DB 301 GCCAGTGTGATGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360

QY 1837 TGTAGCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1896
    |
DB 361 TGTAGCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420

QY 1897 CCCATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1956
    |
DB 421 CCCATTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480

QY 1957 AGCTTTGCCCGATTTCTGCGAGAGCAAGTGTGAGGGGCTCTGGAAGGCTCAAGTCTCA 2016
    |
DB 481 AGCTTTGCCCGATTTCTGCGAGAGCAAGTGTGAGGGGCTCTGGAAGGCTCAAGTCTCA 540

QY 2017 GGAAGCATGGGATTAAGGAAGGATGATGATGATGATGATGATGATGATGATGAT 2076
    |
DB 541 GGAAGCATGGGATTAAGGAAGGATGATGATGATGATGATGATGATGATGATGAT 600

QY 2077 AATTGTTGTAATTAATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATG 2136
    |
DB 601 AATTGTTGTAATTAATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATG 660

QY 2137 GCGCAGCCATTTACATGAGAGCAAGAGGTTTTCACACCTGATGAATGATGATGATG 2196
    |
DB 661 GCGCAGCCATTTACATGAGAGCAAGAGGTTTTCACACCTGATGAATGATGATGATG 720

QY 2197 GCGTGGCTGCAATGAGAGCAAGTGTGATGATGATGATGATGATGATGATGATGATG 2255
    |
DB 721 GCGTGGCTGCAATGAGAGCAAGTGTGATGATGATGATGATGATGATGATGATGATG 780

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QY 2256 CAGAGATTGAGGCTGCGAGCCAGCATGATGATGATGATGATGATGATGATGATGATG 2315
    |
DB 781 CAGAGATTGAGGCTGCGAGCCAGCATGATGATGATGATGATGATGATGATGATGATG 840

QY 2316 ACTGAGACCTGCTCTTAAAGAAAAAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCT 2375
    |
DB 841 ACTGAGACCTGCTCTTAAAGAAAAAAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTG 899

QY 2376 GCGCAGCAT-TGACCCACATGAGGA 2399
    |
DB 900 GCGCAGCATGAGGACCCACATGAGGA 924

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RESULT 3
B0052380/c
LOCUS
DEFINITION B0052380 1075 bp mRNA linear EST 29-MAR-2002
AGENCOURT-6668432 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5933653
5', mRNA sequence.
ACCESSION B0052380
VERSION B0052380.1 GI:19811720
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
TITLES NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@pds.fda.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM2118 row: 1 column: 14
High quality sequence start: 11
High quality sequence stop: 706.
Location/Qualifiers
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FEATURES

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source
1..1075
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5933653"
/clone_lib="NIH_MGC_106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: blood; Vector: pORF7; Site: 1; XhoI: Site 2; EcoRI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCGACGAC(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT      249 a      312 c      259 g      253 t      2 others
ORIGIN

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Query Match      32.1% Score 839.8; DB 14; Length 1075;
Best Local Similarity 94.1%; Pred. No. 9.5e-127;
Matches 948; Conservative 0; Mismatches 49; Indels 10; Gaps 7:

QY 1615 GGAATTTTCAGAACTAGATGATGATGATGATGATGATGATGATGATGATGATG 1671
    |
DB 1060 GGAATTTTCAGAACTAGATGATGATGATGATGATGATGATGATGATGATGATG 1001

QY 1672 -TCAGCTAGACCTCCCTCCCGAGAGGGGCTGCTCTT--CCGCACTCCGAC 1728
    |
DB 1000 TCAGCTTAGACCTCTTTTTCAGAGAGGGGCTGCTCTTCCCATTTCCGAC 941

QY 1729 CTCAATTCCTGGGCCCAAC-GGGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1787

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[illegible]

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC).
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM202 row: d column: 12
High quality sequence step: 657.

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480027"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC library."

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BASE COUNT	231 a	303 c	260 g	228 t
ORIGIN				

Query Match	31.08;	Score 811;	DB 14;	Length 1022
Best local similarity:	0.47			

Best Local Similarity	94.58;	Pred. No.	4.5e-122
Matches	919;	Conservative	0;
		Mismatches	40

Matches	919;	Conservative	0;	Mismatches	40;	Indels	14;	Gaps	7;
---------	------	--------------	----	------------	-----	--------	-----	------	----

[illegible][illegible]

20
 1 TTTGTTGGTCTCCCGGTCTGCCAGCTCTGGCTTC 60

808 AGAAACCCGAGCATCTTTCTGCAGAGGGCTTCTGAGAGGAGGATGCTGCTGA 86

[illegible]

.....CCGCGCCTTTCAGGAGGAGGATGGTGCTGCCTGA 12

868 GTCA~~CC~~CATGAAGACAGGACAGTGCCTCAGCCTGAGGCTGAGACTGCGGATGTCCTGG 92

Db 121 GTCAACCATGAGACAGGACAGTCTTCAGCCTGAGGCTGAGACTCCGCCATCCTCCTCC 18

[illegible]

xy 528 GGUCCTGCTGAGGAGGCTGGCACCCCTGTAGGGAACGGGGTCTTCAAGTTAGCTCA 98

Db 181 GGCTCTGTCAGGAGGAGTGGCAGCCCTGTAGGGAACGGGGTCCCTTCAAGTTAGCTCA 24

[illegible][illegible]

Db 241 GGAGGCTTGAAGCATCACCTCAGGCCAGGTGCAGTGGCTCAGCCTATGATCCAGCA 30

[illegible][illegible]

301 CTTTGGGAGGCTGAGGCCGGTGATCACCCTGAGGTTAGGAGTTCGAGACCAGCCTGGCCA 36

QY 1108 ACATGTTAAACCCCATCTCTACTAAAAATACAGAAATTAGCCGGCGGTGGCGGCA 11

ACATCCTAAAGCCCGTTCCTGCTGGTTAATTAATGTTGGTGTTGCTGGGTGGG

204 ACAGAACCCATCTCTACAAAAACAGAAATAGCCGGGGCGGTGGCGGGCA 42

QY 1168 CCTATAGTCCCAGCTACTCAGAAGCCCTGAGGCTGGGAATCGTTTGAACCCGGGAGCGG 12

[illegible][illegible]

1228 AUGTTCACGGGAGCCGAGATCAGCCACTGCCTCCAGCCTGGGCGACAGAGCGAGAGTC 1235

Db 481 ACGTTCAGGAGCCGAGATCAGCCACTGCACTCCAGCCTGGGCGACAGAGGAGAGTC 540

0x 1288 TGTCTCAAAACCAAATAAATCCAGCGCGGTTT

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location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/node_Organ="blood; Vector: pOT87"
/site_1:XhoI; site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCCGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

```

Superscript II RT (Life Technologies). Note: this is a
Nih_MGC Library."

BASE COUNT 216 a 328 c 297 g 212 t

ORIGIN

Query Match 31.0%: Score 810.8; DB 14; Length 1053;
Best Local Similarity 92.0%: Pred. No. 4, 8e-122;
Matches 957; Conservative 0; Mismatches 67; Indels 16; Gaps 9

QY 287 TCTCCAGGAGGATATGCTCTTTCGGTGCACAGCTGAGACGCCAGAGACC-----TGC 340
DB 1053 TCCCAAGGGGGGAAAGGCCCTCTGGGTCACCACTGGAGACACCCCGAGACCCCTGTGTGG 994
QY 341 TGGGAGCACCCGAGAGAGAGACCCCTGGCCCTTGGAG--TCCCTGATGTGGGATGAAG-C 397
DB 993 GGACCCCCCAAGAAAGAGGCCCTCCGGGCCCTTGGAGTCCCGATTTGGCGGATGAAGCC 934
QY 398 CCACTTAAACAGG-CGCGTGTGGGCTGTGTCTGTAAGCCAAAGTGGGCTGAGCCCTGGCAGC 456
DB 933 CCAATTAAACAGGCCCCGCTGTGGCTGTCTTAAAGCCAAAGGGGGGTGAGCCCTGCAGC 874
QY 457 ATGACCCCTGCG-AAGGGGCCCTGTGCTCTTCAGAGCCCC--ACCACTAGACATCGAGGC 513
DB 873 AAGACCTCGGAAAGGGGGCCCTGTCTTTCAGCCCCCCCCACCAATTAAGACTCTTGAGGC 814
QY 514 TCTTTTCGGG-CCAACTTCTCTAGTATGCCCTCACAGCCGCGAGCCCTCCCTGACCTGCA 572
DB 813 TCTTTTCGGGCCCAAGTCTCTCTAGTGCCTTCACAGCCGCGAGCCCTCTTTCGACTTGA 754
QY 573 GG-CCAAGAGACAGAGGACGAGATTTGGGAAAGCCCTCTCCGAAAGGTGTGTCCCTTC 631
DB 753 GGCCCAAGAGACAGAGGACGAGGGGTGTGAAAGCCCTCTCTCCATGGTGTCTCTTC 694
QY 632 GGAAGGCTGGCTGGGATGAGAGCTTGGGGCATGCTGGGGCAATCCCTGACTCTCTGTG 691
DB 693 GGAAGGCTGGCTGGGATGAGAGCTTGGGGCATGCTGGGGCAATGCTCTCTCTGTG 634
QY 692 ACCTGGCCCCGCCACGCTGCACCTGCGAGGCTTCTGAGAGCCCTTGGGTTTTTGTGT 751
DB 633 ACCTGGCCCCGCCACGCTGCACCTGCGAGGCTTCTGAGAGCCCTTGGGTTTTTGTGT 574
QY 752 GTTTGTGTTTGTGTGTGTGTGTGTCTCCCGTGAGGCTGTG-CCGAGCTCTGGCTTCAGA 810
DB 573 GTTTGTGTTTGTGTGTGTGTGTGTCTCCCGTGAGGCTGTG-CCGAGCTCTGGCTTCAGA 514
QY 811 AAACCCCAACATCTTTTCTGCAGAGGGGCTTCTGAGAGAGAGGATGCTGCTGAGTC 870
DB 513 AAACCCCAACATCTTTTCTGCAGAGGGGCTTCTGAGAGAGAGGATGCTGCTGAGTC 454
QY 871 ACCCAATGAAGACAGACAGTGTTCAGCTTGAAGCTGAGACTGCGGGATGCTCTGAGGC 930
DB 453 ACCCAATGAAGACAGACAGTGTTCAGCTTGAAGCTGAGACTGCGGGATGCTCTGAGGC 394
QY 931 TCTGTGTAGGGAGAGGTGTGAGCCCTTATAGGAAAGGGGGTCTTCAAGTTAGTACAGGA 990
DB 393 TCTGTGTAGGGAGAGGTGTGAGCCCTTATAGGAAAGGGGGTCTTCAAGTTAGTACAGGA 334
QY 991 GCGTTGGAAGACATCACTCAAGCCAGGTGCAAGTGTCAAGCTTATGATCCAGCACTT 1050
DB 333 GCGTTGGAAGACATCACTCAAGCCAGGTGCAAGTGTGCAAGCTTATGATCCAGCACTT 274
QY 1051 TGGGAGGCTGAGAGGGGGGTGATCACTCTGAGGTTAGGAGTTTCAGAGCAAGCTTGGCCAA 1110
DB 273 TGGGAGGCTGAGAGGGGGGTGATCACTCTGAGGTTAGGAGTTTCAGAGCAAGCTTGGCCAA 214
QY 1111 TGGTAAACCCCACTCTACTAAAAATACAGAAATTAAGCCGGGCGTGTGGCGGACCT 1170
DB 213 TGGTAAACCCCACTCTACTAAAAATACAGAAATTAAGCCGGGCGTGTGGCGGACCT 154
QY 1171 ATATCCACAGTATCTCAGAGAGCTGAGAGCTGGGAAATCTGTTTAACCCGGGAAAGCGGAGG 1230
DB 153 ATATCCACAGTATCTCAGAGAGCTGAGAGCTGGGAAATCTGTTTAACCCGGGAAAGCGGAGG 94

[illegible]

RESULT 6	
B0690571	945 bp mRNA linear EST 15-JUL-2002
LOCUS	
DEFINITION	AGENCOURT 8342072 NTH_MGC_110 Homo sapiens cDNA clone IMAGE:6248991 5' , mRNA sequence.

VERSION	BO690571.1	GI:21815867
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
REFERENCE	1 (bases 1 to 945)	
AUTHORS	Mammalia; Euteleia; Primates; Catarrhini; Homiidae; Homo.	
TITLE	NH-MGC http://mgc.ncl.nih.gov/ .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	

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FEATURES
source
    cDNA Library Preparation: Rubin Laboratory
    cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
    DNA Sequencing by: Agencourt Bioscience Corporation
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LNLN at:
    http://image.llnl.gov
    plate: LCM2389 row: 1 column: 16
    High quality sequence stop: 588.
    location/Qualifiers
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BASE COUNT
BRIGIN

205 a 244 c 290 g 205 t 1 others

/organism="Homo sapiens"
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 /clone="IMAGE:6248991"
 /clone_1fb="NH_MGC_110"
 /issue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pOMB7; Site:1: XhoI;
 Site:2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAC(C). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NH_MGC library."

Query Match	30.5%	Score 797.2	DB 14	Length 945
Best Local Similarity	97.3%	Pred. No. 8.1e-120		
Matches 853	Conservative	0	Mismatches 19	Indels 5
				Gaps 4
QY	1659	CTCTACTCTTACCTACGCTTACGACCTTCTCTCTCTCCACAGAGGGGTGGGTTCTCTTCCC	1718	
DB	1	CTCTACTCTTACCTACGCTTACGACCTTCTCTCTCCACAGAGGGGTGGGTTCTCTTCCC	60	
QY	1719	CACCTCCACCACTTCAATTCCTGTGGGCCCAACGAGGCTGACCTGACATTTGGTACATGGC	1778	
DB	61	CACCTCCACCACTTCAATTCCTGTGGGCCCAACGAGGCTGACCTGACATTTGGTACATGGC	120	
QY	1779	CAGTGTGATTCACAAATGGCAGTCTGTGTCTGGGCTCTGTGTTCGCTGTGCGTGGGTGTGG	1838	
DB	121	CAGTGTGATTCACAAATGGCAGTCTGTGTCTGGGCTCTGTGTTCGCTGTGCGTGGGTGTGG	180	
QY	1839	TAGCCAAAGTCGATTAAGTTGAATGGCTTGCCTTGAAGCCACTGAACCTGGGATTTCTCTCC	1898	

Db	181	TACCCAGAGTCGGTAAGTTGAATGATGCGCTTGCCTTTGAAAGCCACTGAAGCTGGGATTCCTCC	240
Qy	1899	CATTAGAGTCAGCCCTTCCTCCCTCCAGAGGCGCAGAGGCCCTTCGACAGAGGGAACCAAGTGTAG	1958
Db	241	CATTAGAGTCAGCCCTTCCTCCCTCCAGAGGCGCAGAGGCCCTTCGACAGAGGGAACCAAGTGTAG	300
Qy	1959	CGTTGCCCGGATTTCTGGGAGGAACGAGTTTGAGGGGCTCTCTGGAAAAGCTAGTCTCAGG	2018
Db	301	CGTTGCCCGGATTTCTGGGAGGAACGAGTTTGAGGGGCTCTCTGGAAAAGCTAGTCTCAGG	360
Qy	2019	AGCATGGGGATTAAGAGAGAGGCATGATAAATTGTCTTAGCAGACAGAGGCGCAGGGTGTATAA	2078
Db	361	AGCATGGGGATTAAGAGAGAGGCATGATAAATTGTCTTAGCAGACAGAGGCGCAGGGTGTATAA	420
Qy	2079	TTGTGTTAAATTCACCTGACCTTGACCTTGGCAGCTGACCTAATTGAGGCTGGGAGAC	2138
Db	421	TTGTGTTAAATTCACCTGACCTTGACCTTGGCAGCTGACCTAATTGAGGCTGGGAGAC	480
Qy	2139	CCAGCCATTACCATGAGACAAAGAGGTTTTCACCCCGGATTCAGATTCAGATTCAGACTGG	2198
Db	481	CCAGCCATTACCATGAGACAAAGAGGTTTTCACCCCGGATTCAGATTCAGATTCAGACTGG	540
Qy	2199	CTGGCTGCAGTGAAGCTGACCTGTACTCAGAGGCTGAGGGGAGAGATTCATGAGGCCAG	2258
Db	541	CTGGCTGCAGTGAAGCTGACCTGTACTCAGAGGCTGAGGGGAGAGATTCATGAGGCCAG	600
Qy	2259	GAGTTTGAAGCTGAGAGGAGCTATGATTCGGCCACTACACTCCAGCCCTGAGAACACAGT	2318
Db	601	GAGTTTGAAGCTGAGAGGAGCTATGATTCGGCCACTACACTCCAGCCCTGAGAACACAGT	660
Qy	2319	GAGACCTGTCTCTTTAAAGAAAAAAAAGCTGACCTGCTGGGAGCTGGCCAGAGTTTCTGCC	2378
Db	661	GAGACCTGTCTCTTTAAAGAAAAAAAAGCTGACCTGCTGGGAGCTGGCCAGAGTTTCTGCC	719
Qy	2379	CACATTGGACCCACATGAGAGACATGATGAGAGCCGACCTG - CCCCCTGGTGGACAGTCTT -	2436
Db	720	CACATTGGACCCACATGAGAGACATGATGAGAGCCGACCTG - CCCCCTGGTGGACAGTCTT -	779
Qy	2437	GGGAGAACCTCAGGCTTCCTTGGCATCAGAGGCGCAGAGCCGGGAGG - GCAGTAAATTGG	2494
Db	780	GGGAGAACCTCAGGCTTCCTTGGCATCAGAGGCGCAGAGCCGGGAGGAAAGCAATGAATTGG	839
Qy	2449	AGACTGTGGGGCTTGGTTCCCTTGTGTGTGTGTG 2531	
Db	840	AGACTGTGTGGGGCTTGGTTCCCTTGTGTGTGTGTGTG 876	

RESULT 7	BI838021	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	BI838021		771 bp	MRNA	linear	EST 04-OCT-2001							
	603083896F1	NIH-MGC_120	Homo sapiens	cDNA clone	IMAGE:5222896 5',								
	BI838021			MRNA sequence.									
	BI838021.1	GI:15949571		EST.				human.					
								Homo sapiens					
								Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;					
								Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
								1 (bases 1 to 771)					
								NIH-MGC http://mgc.nci.nih.gov/ .					
								National Institutes of Health, Mammalian Gene Collection (MGC)					
								Unpublished (1999)					
								Contact: Robert Strausberg, Ph.D.					
								Email: cgapbs-remail.nih.gov					
								Tissue Procurement: Life Technologies, Inc.					
								cDNA Library Preparation: Life Technologies, Inc.					
								DNA Sequencing by: Incyte Genomics, Inc.					
								Clone distribution: MGC clone distribution information can be					
								found through the I.M.A.G.E. Consortium/LLNL at:					
								http://image.llnl.gov					
								Place: LLNL1560					
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LOCUS A1935824/c
DEFINITION w51c01.x1 NCI-CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2458848 3'
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(HUMAN); contains Alu repetitive element.; mRNA sequence.
ACCESSION A1935824
VERSION A1935824.1 GI:5674694
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 697)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.illn.gov/db/ftp/image/image.html
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BASE COUNT 150 a 211 c 166 g 170 t
ORIGIN

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Best Local Similarity 98.7%; Pred. No.3.5e-101;
Matches 688; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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mRNA sequence.
ACCESSION B1911067 GI:16174604
VERSION B1911067
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 759)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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DB	477	TGTTATTAATTCACACAGGACCTTGAAGCTTGGACGTAATTTGGAGGCTGGACAGCC	Human	Chromosome 1	111	TGTTATTAATTCACACAGGACCTTGAAGCTTGGACGTAATTTGGAGGCTGGACAGCC	418	
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OY	2259	GAGTT-TGAGGCTGAGCAGCAGCTATGATTCGGCCCACTACCTCCAGCCTGACACAGAG	Human	Chromosome 1	111	GAGTT-TGAGGCTGAGCAGCAGCTATGATTCGGCCCACTACCTCCAGCCTGACACAGAG	2317	
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DEFINITION	1128d03.y1 HR85 Islet Homo sapiens cDNA clone IMAGE:6031157 5'							
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VERSION	B0632819.1							
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AUTHORS	Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Keestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wille, T., Martin, J., Blisstein, A., Smith, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsengarelshvili, R., Williams, T., Jackson, Y., and Bowers, Y.							
TITLE	Endocrine Pancreas Consortium							
JOURNAL	Unpublished (2000)							
COMMENT	Other: ESTs: 1128d03.x1 Contact: Douglas Melton, Klaus H. Keestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohpc.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 484. Location/Qualifiers							

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SOURCE       human.
ORGANISM     Homo sapiens
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              1 (bases 1 to 672)
AUTHORS      Gonzalez, P., Epstein, D.L. and Borras, T.
TITLE        Characterization of gene expression in human trabecular meshwork
              using single-pass sequencing of 1060 clones
JOURNAL      Invest. Ophthalmol. Vis. Sci., (2000) In press
COMMENT      Contact: Pedro Gonzalez
              Department of Ophthalmology
              Duke University
              Duke Eye Center, Erwin Rd, Box 3802, Durham, NC 27710-3802, USA
              Tel: 919 681 4085
              Fax: 919 684 8983
              Email: pedro.gonzalez@duke.edu.
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ACCESSION  A1813532
VERSION    A1813532.1 GI:5424738
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 733)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Life Technologies catalog #: 11547-015
              DNA Sequencing by: Washington University Genome Sequencing Center
              Clone distribution: NCI-CGAP clone distribution information can be
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 Job time : 5067.06 secs

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8  : APPLICANT: WALLACH, David
9  :
10 : APPLICANT: BIDA, Jaek
11 :
12 : APPLICANT: BELETSEVY, Igor
13 :
14 : APPLICANT: METT, Igor
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16 : TITLE OF INVENTION: TNF LIGANDS
17 :
18 : NUMBER OF SEQUENCES: 17
19 :
20 : CORRESPONDENCE ADDRESS:
21 :
22 : ADDRESSEE: BROWDY AND NETKAMP
23 :
24 : STREET: 419 Seventh Street, N.W.
25 :
26 : CITY: Washington
27 :
28 : STATE: D.C.
29 :
30 : COUNTRY: USA
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9  FILING DATE:
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: IL 106271
12 FILING DATE: 08-JUL-1993
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Townsend, G. Kevin
15 REGISTRATION NUMBER: 34,033
16 REFERENCE/DOCKET NUMBER: WALLACH-10
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 202-628-5197
19 TELEFAX: 202-737-3528
20 TELEX: 248633
21 INFORMATION FOR SEQ ID NO: 2:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 2224 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single
26 TOPOLOGY: linear
27 MOLECULE TYPE: CDNA
28 FEATURE:
29 NAME/KEY: CDS
30 LOCATION: 90..1472
31 US-08-477-347-2

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QY	157	AATGTCACCTGCATGCTGTAACCTCTGTAGCAGCTGTGACACACAGCTCACAGTCTCTTC	216
Db	1227	AATGTCACCTGCATGCTGTAACCTCTGTAGCAGCTGTGACACACAGCTCACAGTCTCTTC	1286
QY	217	CAAGCCAGCTCCACATGGAGAGACACAGATTCTCAGCCCCCTCGAGTCCCGGAAGACGAG	276
Db	1287	CAAGCCAGCTCCACATGGAGAGACACAGATTCTCAGCCCCCTCGAGTCCCGGAAGACGAG	1346
QY	277	CAGGTCCTCTTCCAGAGGAGAAATGTGCTTTCGTGTCACAGCTGAGAGCCAGAGACC	336
Db	1347	CAGGTCCTCTTCCAGAGGAGAAATGTGCTTTCGTGTCACAGCTGAGAGCCAGAGACC	1406
QY	337	CTGCTGGGGAGACCGAAGAAAGCCCTTGCCCTTGGAGTCCCTGATCTGGATGAAG	396
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Db	1587	TTCCTGGGGCAACTTCTCTCTAGTCCCTCCACAGCCGACCTCCCTCTGACCTCGAGGCC	1646
QY	577	AAGACAGAGGAGGAGATTGGGAAAGCCTCTGCTGCATGATGTTGTCCTCTCGGAAG	636
Db	1647	AAGACAGAGGAGGAGATTGGGAAAGCCTCTGCTGCATGATGTTGTCCTCTCGGAAG	1706
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1  RESULT 4 8-862-1
2  US-08-476-862-1
3  : Sequence 1, Application US/08476862
4  : Patent No. 6262239
5  :
6  : GENERAL INFORMATION:
7  : APPLICANT: WALLACH, David
8  : APPLICANT: BIGDA, Jacek
9  : APPLICANT: BELETSKY, Igor
10 : APPLICANT: METT, Igor
11 : APPLICANT: ENGELMANN, Hartmut
12 : TITLE OF INVENTION: TNF INHIBITORS
13 : NUMBER OF SEQUENCES: 8
14 :
15 : CORRESPONDENCE ADDRESS:
16 : ADDRESSEE: BROWDY AND NEWMARK
17 : STREET: 419 Seventh Street, N.W.
18 : CITY: Washington
19 : STATE: D.C.
20 : COUNTRY: USA
21 :
22 : ZIP: 20004
23 :
24 : COMPUTER READABLE FORM:
25 : MEDIUM TYPE: Floppy disk
26 : COMPUTER: IBM PC compatible
27 : OPERATING SYSTEM: PC-DOS/MS-DOS
28 : SOFTWARE: PatentIn Release #1.0, Version #1.25
29 :
30 : CURRENT APPLICATION DATA:
31 : APPLICATION NUMBER: US/08/476,862
32 : FILING DATE: 07-JUN-1995
33 : CLASSIFICATION: 435
34 :
35 : PRIOR APPLICATION DATA:
36 : PRIOR APPLICATION NUMBER: IL 107267
37 : FILING DATE: 12-OCT-1993
38 :
39 : PRIOR APPLICATION DATA:
40 : APPLICATION NUMBER: IL 94039
41 : FILING DATE: 06-APR-1990
42 :
43 : PRIOR APPLICATION DATA:
44 : APPLICATION NUMBER: IL 91229
45 : FILING DATE: 06-AUG-1989

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PROR APPLICATION DATA: IL 90339
 APPLICATION NUMBER: 18-MAY-1989
 FILING DATE: 18-MAY-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, ROGER L.
 REGISTRATION NUMBER: 25, 618
 REFERENCE/DOCKET NUMBER: WALLACH-12A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2224 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 90..1472
 US-08-476-862-1

LOCATION: 90..1472
US-08-476-862-1

Query Match	39.6%;	Score 1034;	DB 4;	Length 2224;
Best Local Similarity	98.6%;	Pred. No. 7.6e-267;		
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				Gaps 0;

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QY	157	AATGTCACCTGCATGATGAACCTCTGTATGACACTCTGACCAACAGCTCAACAGTCTCTCC	216
DB	1227	AATGTCACCTGCATGATGAACCTCTGTATGACACTCTGACCAACAGCTCAACAGTCTCTCC	1286
QY	217	CAAGCCAGCTCCACAATGGGAGACACACATTCACAGCCCTCGGAGTCCCGGAAGACGAG	276
DB	1287	CAAGCCAGCTCCACAATGGGAGACACACATTCACAGCCCTCGGAGTCCCGGAAGACGAG	1346
QY	277	CAGGTCGCCCTTCCAAAGAGAGAAATGGCTCTTGGTCACTACCTGGAGACGCCAGAGACC	336
DB	1347	CAGGTCGCCCTTCCAAAGAGAGAAATGGCTCTTGGTCACTACCTGGAGACGCCAGAGACC	1406
QY	337	CTGCTGGGGAGACCCGAAAGAAAGCCCTCGCCCTTGGAGTGCCTGATGCTGGATGAAG	396
DB	1407	CTGCTGGGGAGACCCGAAAGAAAGCCCTCGCCCTTGGAGTGCCTGATGCTGGATGAAG	1466
QY	397	CCGAGTTAAACAAGGCGCGTGGGCGTGTGCTGACGCAAGGTGGGTGAGCCCTGGCAGG	456
DB	1467	CCGAGTTAAACAAGGCGCGGTGTGGGCTGTGCTGACGCAAGGTGGGTGAGCCCTGGCAGG	1526
QY	457	ATGACCCCTGCGAAGGGGGCCCTGCTCTTCACAGGCCCCCAACACTAGAGACTGTAGAGCTT	516
DB	1527	ATGACCCCTGCGAAGGGGGCCCTGCTCTTCACAGGCCCCCAACACTAGAGACTGTAGAGCTT	1586
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DB	1587	TTCCTGGGCCAAATTCCTCTAGTGGCCCTCCACACGCCGACGCTCCTCTGACTGCAAGGCC	1646
QY	577	AAGACGACAGGAGGAGGATGGGGAAAGCCTGCGTGCATGATGTGTCCTCTCGGAAG	636
DB	1647	AAGACGACAGGAGGAGGATGGGGAAAGCCTGCGTGCATGATGTGTCCTCTCGGAAG	1706
QY	637	GCTGCGTGGGCATGACATTCGCGGGCATGCTGGGGCAAGTCCCTGCACTCTGTGCACTG	696
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1  OPERATING SYSTEM: PC-DOS/MS-DOS
2  SOFTWARE: Patentin Release #1.0, Version #1.25
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: US/08/650,000
5  FILING DATE:
6  CLASSIFICATION: 435
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER: US/08/468,453
9  FILING DATE:
10 APPLICATION NUMBER: US/08/038,765
11 FILING DATE:
12 APPLICATION NUMBER: US 403,241
13 FILING DATE: 05-SEP-1989
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 405,370
16 FILING DATE: 11-SEP-1989
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 421,417
19 FILING DATE: 13-OCT-1989
20 APPLICATION DATA:
21 APPLICATION NUMBER: US 523,635
22 FILING DATE: 10-MAY-1990
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Wight, Christopher L.
25 REGISTRATION NUMBER: 31,680
26 REFERENCE/DOCKET NUMBER: 2501-D
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (206) 587-0430
29 TELEFAX: (206) 233-0644
30 INFORMATION FOR SEQ ID NO: 1:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 1641 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: cDNA to mRNA
37 HYPOTHEICAL: NO
38 ANTI-SENSE: NO
39 ORIGINAL SOURCE:
40 ORGANISM: Homo sapiens
41 CELL TYPE: Fibroblast
42 CELL LINE: WI-26 VAA
43 IMMEDIATE SOURCE:
44 LIBRARY: WI-26 VAA
45 CLONE: 1
46 FEATURE:
47 NAME/KEY: CDS
48 LOCATION: 88..1473
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53 NAME/KEY: sig_peptide
54 LOCATION: 88..153
55 PUBLICATION INFORMATION:
56 AUTHORS: Smith, Craig A.
57 AUTHORS: Davis, Terri
58 AUTHORS: Anderson, Dirk
59 AUTHORS: Solam, Lisabell
60 AUTHORS: Beckmann, M. P.
61 AUTHORS: Jerzy, Rita
62 AUTHORS: Cosman, Steven K.
63 AUTHORS: Goodwin, Raymond G.
64 TITLE: A Receptor for Tumor Necrosis Factor Defines
65 TITLE: an Unusual Family of Cellular and Viral Proteins
66 JOURNAL: Science
67 VOLUME: 248
68 PAGES: 1019-1023
69 DATE: 25-MAY-1990
70 US-08-650-000-1

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QY	217	CAAGCCAGCTCCAAATGGGAGACACAGATTCCAGGCCCTCGAGTCCCGCAAGACAG	276
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: APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,			
: M. PATRICIA			
: TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR- α AND			
: B-RECEPTORS			
: NUMBER OF SEQUENCES: 17			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/07/523,635			
: FILING DATE: 10-MAY-1990			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: 421,417			
: FILING DATE: 13-OCT-1989			
: APPLICATION NUMBER: 405,370			
: FILING DATE: 11-SEP-1989			
: APPLICATION NUMBER: 403,241			
: FILING DATE: 05-SEP-1989			
: SEQ ID NO: 1:			
: LENGTH: 1641			
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Best Local Similarity 96.9%; Pred. No. 1.7e-111;			
Matches 462; Conservative 0; Mismatches 15; Indels 0; Gaps 0;			
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Db	1225	AATGTACCTGCATCGTGAACGTCGTGTACAGTCTGACACAGCTCACAGTCTCTCC	1284
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QY	397	CCCAGTTAACACAGCGCGGTGTGTGTCTGTAAGCCAAAGTGGCGTGAAGCCCTGGCAG	456
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: Patent No. 5395760			
: APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,			
: M. PATRICIA			
: TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR- α AND			
: B-RECEPTORS			
: NUMBER OF SEQUENCES: 17			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/07/523,635			
: FILING DATE: 10-MAY-1990			


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Db 64929 CCCGTTCTATTAAATAATTAAGCCGGCATGTGCGAGGACCTGTATATCC 64870
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According to the Pre Publication Rules, every patent application received by the United States Patent and Trademark Office after November 29, 2000 will be pre-published at eighteen months from the effective filing date. When the application is published the contents, including the sequences, will become prior art.

Two new databases have been created to hold the pre-published sequences:

Published_Applications_NA contains nucleic acid sequences; the search results will have the extension **.rnpb**.

Published_Applications_AA contains amino acid sequences; the search results will have the extension **.rapb**.

Each pre-published application is given a unique Publication Number. An example of a Publication Number is US20021234567A1. The "US" indicates the application was a U.S. application. The first 4 digits show the calendar year the application was published. The next 7 digits represent when the application was published. This 7-digit number starts at zero at the beginning of each calendar year. Each application published is given the next number in order. The "A" indicates a utility patent application and the "1" shows that this was the first time the application had been published. If the applicants submit changes to the application, they may request that the changed application be published again. In such instances, the "1" at the end of the number would be replaced by a "2".

Sequences in the PGPub database are public information; it is permissible to leave these results in the case.

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Qy 2497 ACTCTGTGGGCGCTTGTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 2556
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Db 3567 ACTCTGTGGGCGCTTGTCCCTTGTGTGTGTGTATCCCAAGACATGAAGTTTG 3626
|||
Qy 2557 CACTGTATGCTGAGCGCATTCCTGCTATCAATAAACCTGTTTAAAAAAA 2613
|||
Db 3627 CACTGTATGCTGAGCGCATTCCTGCTATCAATAAACCTGTTTAAAAAAA 3683
|||

RESULT 2

US-09-800-909-1
: Sequence 1. Application US/09800909
: Patent No. US20010019833A1
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BIGDA, Jacek
: APPLICANT: BELETSKY, Igor
: APPLICANT: MERT, Igor
: APPLICANT: ENGELMANN, Hartmut
: TITLE OF INVENTION: TNF INHIBITORS
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BROWDY AND NEIMARK
: STREET: 419 Seventh Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/800.909
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/476.862
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 94039
: FILING DATE: 06-APR-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 91229
: FILING DATE: 06-AUG-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IL 90339
: FILING DATE: 18-MAY-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: WALLACH-12A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:

: LENGTH: 2224 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 90..1472
: US-09-800-909-1

Query Match 39.6%; Score 1034; DB 10; Length 2224;
Best Local Similarity 98.6%; Pred. No. 9,6e-211;
Matches 1043; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 97 GACCCCAACCCATCTTGTGCTTAGACAGATTTCTCCCTGGTGGCCATGGAGCCAGCTC 156
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Db 1167 GAGGCCCGGCAGACCCGAGAGCTCAGATTTCTCCCTGGTGGCCATGGAGCCAGCTC 1226
|||
Qy 157 AATGTACCTGATCGTGAAGCTGTAGACGCTGACCCAGCTCAGAGCTCAGAGTCTCTCC 216
|||
Db 1227 AATGTACCTGATCGTGAAGCTGTAGACGCTGTGACGCTGACCCAGCTCAGAGTCTCTCC 1286
|||
Qy 217 CAAGCAGCTCCAGCATGGAGACACAGATTCAGCCCTTGGAGTCCCGAAGAGCAG 276
|||
Db 1287 CAAGCAGCTCCAGCATGGAGACACAGATTCAGCCCTTGGAGTCCCGAAGAGCAG 1346
|||
Qy 277 CAGTCCCTTCTCCAGAGGAATGTCCCTTGTGTCACAGCTGAGAGCCAGAGACC 336
|||
Db 1347 CAGTCCCTTCTCCAGAGGAATGTCCCTTGTGTCACAGCTGAGAGCCAGAGACC 1406
|||
Qy 337 CTGCTGGGAGACACGAAAGAACGCCCTGCTGAGAGCCTGAGTCTGGATATAG 396
|||
Db 1407 CTGCTGGGAGACACGAAAGAACGCCCTGCTGAGAGCCTGAGTCTGGATATAG 1466
|||
Qy 397 CCAGTTAACAGGCGGCTGTGGCTGTGTGTAGCCAAAGTGGGCTGAGCCCTGAGCAG 456
|||
Db 1467 CCAGTTAACAGGCGGCTGTGGCTGTGTGTAGCCAAAGTGGGCTGAGCCCTGAGCAG 1526
|||
Qy 457 ATGACCTTGGCAAGGGGCGCTGTGCTTTCAGAGCCCGACCATAGAGCTGTGAGGCTCT 516
|||
Db 1527 ATGACCTTGGCAAGGGGCGCTGTGCTTTCAGAGCCCGACCATAGAGCTGTGAGGCTCT 1586
|||
Qy 517 TTCTGGGCAAGTTCTCTAGTGCCTCCACAGCGGAGGCTCCCTGACCTCCAGGCC 576
|||
Db 1587 TTCTGGGCAAGTTCTCTAGTGCCTCCACAGCGGAGGCTCCCTGACCTCCAGGCC 1646
|||
Qy 577 AAGAGCAGAGCAGCGAGTTGGGAAAGCCCTCTGCTGCATGATGTCTCCCTTCGGAAG 636
|||
Db 1647 AAGAGCAGAGCAGCGAGTTGGGAAAGCCCTCTGCTGCATGATGTCTCCCTTCGGAAG 1706
|||
Qy 637 GCTGGCTGGGATGAGAGCTTGGGGCATGTGGGGCAAGTCCCTGACTCTGTGACCTG 696
|||
Db 1707 GCTGGCTGGGATGAGAGCTTGGGGCATGTGGGGCAAGTCCCTGACTCTGTGACCTG 1766
|||
Qy 697 CCGCGCCAGCTGCACCTGCCAGCCTGGCTTCTGGAGCCCTTGGGTTTGTGTTG 756
|||
Db 1767 CCGCGCCAGCTGCACCTGCCAGCCTGGCTTCTGGAGCCCTTGGGTTTGTGTTG 1826
|||
Qy 757 TTTGTTGTTGTTGTTGTTCTCCCTGTGGGCTGTGCCAGCTGTGCTTCAGAAAAACC 816
|||
Db 1827 TTTGTTGTTGTTGTTGTTCTCCCTGTGGGCTGTGCCAGCTGTGCTTCAGAAAAACC 1886
|||
Qy 817 CAGCATCTTTTTCGAGAGGGGCTTCTGAGAGGAGAGGATGTGCTGATGACCAT 876
|||
Db 1887 CAGCATCTTTTTCGAGAGGGGCTTCTGAGAGGAGAGGATGTGCTGATGACCAT 1946
|||
Qy 877 GAAGACAGAGCAGTCTTCAAGCTGAGGCTGAGACTCGGAGATGTCTCTGGGCTGTG 936
|||
Db 1947 GAAGACAGAGCAGTCTTCAAGCTGAGGCTGAGACTCGGAGATGTCTCTGGGCTGTG 2006
|||
Qy 937 TAGGAGAGAGGTGCAGCCCTGTAGGGAAGGGGCTCTTCAAGTTAGCTCAGAGGCTTG 996
|||
Db 2007 TAGGAGAGAGGTGCAGCCCTGTAGGGAAGGGGCTCTTCAAGTTAGCTCAGAGGCTTG 2066
|||

QY 997 GAAGCATCACCTGAGCGAGTGCAGTGGCTACGCCCTATGATCCAGCATTGGAG 1056
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Db 2067 GAAAGCATCACCTGAGCGAGTGCAGTGGCTACGCCCTATGATCCAGCATTGGAG 2126
QY 1057 CCTAGAGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 1116
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Db 2127 GCTAGAGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 2186
QY 1117 AACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 1154
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Db 2187 AACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 2224

RESULT 3

US-09-800-908-2

Sequence 2, Application US/09800908

Patent No. US20020111462A1

GENERAL INFORMATION:

APPLICANT: WALLACH, David

BIGDA, Jacek

BELETSKY, Igor

METT, Igor

TITLE OF INVENTION: TNF LIGANDS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W.

City: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/800.908

FILING DATE: 08-Mar-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/477,347

FILING DATE: <unknown>

APPLICATION NUMBER: IL 106271

FILING DATE: 08-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Townsend, G. Kevin

REGISTRATION NUMBER: 34,033

REFERENCE/DOCKET NUMBER: WALLACH-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

TELEX: 248633

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2224 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 90..1472

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-800-908-2

Query Match 39.6%; Score 1034; DB 10; Length 2224;
Best Local Similarity 98.6%; Pred. No. 9, 6e-211;
Matches 1043; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 97 GACCCCAACCCCATCTGTGCTTACAGATTCTCCCTGGCCATGGAGCCAGGTC 156
||| ||| ||| | |||||||||||||||||||||||||||||||||||||||

Db 1167 GAGGCCCGGGCCAGCACCGGAGACTAGATTCTCCCTGGTGGCCATTGGACCCAGGTC 1226
QY 157 AATGTCACCTGATGTTGATGACCTGTGTACACCTGTGACACACAGCTCAGTCTCC 216
|||||
Db 1227 AATGTCACCTGATGTTGATGACCTGTGTACACCTGTGACACACAGCTCAGTCTCC 1286
QY 217 CAAGCAGCTCCACATGAGGAGACACAGATTCCACCTCTGAGTCTCCGAGAGCAG 276
|||||
Db 1287 CAAGCAGCTCCACATGAGGAGACACAGATTCCACCTCTGAGTCTCCGAGAGCAG 1346
QY 277 CAGGTCCTCTTCCAGAGGAGAAATGTGCTTTTGGGTACACAGCTGAGACGCGAGAGCC 336
|||||
Db 1347 CAGGTCCTCTTCCAGAGGAGAAATGTGCTTTTGGGTACACAGCTGAGACGCGAGAGCC 1406
QY 337 CTGCTGGGGAGACACGGAAGAAGACCCCTGGCCCTTTGAGTCTGATGCTGGATGAG 396
|||||
Db 1407 CTGCTGGGGAGACACGGAAGAAGACCCCTGGCCCTTTGAGTCTGATGCTGGATGAG 1466
QY 397 CCCAGTTAACACAGCGCGGTGGGCTGTGTCTAGCCCAAGGTTGGGCTGAGCCCTGGCAG 456
|||||
Db 1467 CCCAGTTAACACAGCGCGGTGTGGGCTGTGTCTAGCCCAAGGTTGGGCTGAGCCCTGGCAG 1526
QY 457 ATGACCTTCCGAAAGGGGCCCTGTCTTCCAGAGCCGCCACCACTAGAGCTGTGAGGCTCT 516
|||||
Db 1527 ATGACCTTCCGAAAGGGGCCCTGTCTTCCAGAGCCGCCACCACTAGAGCTGTGAGGCTCT 1586
QY 517 TTCTGGGCAAGTTCTCTAGTGGCCCTCCACAGCCGCGACCTCTCTGACTGTGAGGCC 576
|||||
Db 1587 TTCTGGGCAAGTTCTCTAGTGGCCCTCCACAGCCGCGACCTCTCTGACTGTGAGGCC 1646
QY 577 AAGAGCAGAGGAGGAGAGTTGGGGAAGCCCTGCTGCTGATGTTGTTCTCTGCAAG 636
|||||
Db 1647 AAGAGCAGAGGAGGAGAGTTGGGGAAGCCCTGCTGCTGATGTTGTTCTCTGCAAG 1706
QY 637 GCTGCTGGGCAATGACCTGTGGGGCAATGCTGGGCAAGTCCCTACTCTCTGTGACTG 696
|||||
Db 1707 GCTGCTGGGCAATGACCTGTGGGGCAATGCTGGGCAAGTCCCTACTCTCTGTGACTG 1766
QY 697 CCCCGCCAGCTGACACCTGCGACCTGAGCCGCTTGGAGCCCTTGGTTTGTGTTGTTG 756
|||||
Db 1767 CCCCGCCAGCTGACACCTGCGACCTGAGCCGCTTGGAGCCCTTGGTTTGTGTTGTTG 1826
QY 757 TTTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 816
|||||
Db 1827 TTTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1886
QY 817 CAGCATCTCTTCTGACAGAGGGCTTTCTGAGAGAGAGGATGCTGCTGATCACCAT 876
|||||
Db 1887 CAGCATCTCTTCTGACAGAGGGCTTTCTGAGAGAGAGGATGCTGCTGATCACCAT 1946
QY 877 GAAAGCAGAGCAGTGTCTGAGCTGAGGCTGAGAGGAGTGGTCTGGGGGCTCTGTG 936
|||||
Db 1947 GAAAGCAGAGCAGTGTCTGAGCTGAGGCTGAGAGGAGTGGTCTGGGGGCTCTGTG 2006
QY 937 TAGGAGAGAGTGGAGCCCTGTAGGGAACGGGCTCTTCAAGTTAGCTCAGAGAGCTTG 996
|||||
Db 2007 TAGGAGAGAGTGGAGCCCTGTAGGGAACGGGCTCTTCAAGTTAGCTCAGAGAGCTTG 2066
QY 997 GAAAGCATCACCTGAGCGAGTGCAGTGGCTACGCCCTATGATCCAGCATTGGAG 1056
|||||
Db 2067 GAAAGCATCACCTGAGCGAGTGCAGTGGCTACGCCCTATGATCCAGCATTGGAG 2126
QY 1057 GCTGAGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 1116
|||||
Db 2127 GCTGAGCGGTGATCAGCTGAGGTTAGAGATTGAGACCCAGCCTGGCCAACTGTAA 2186
QY 1117 AACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 1154
|||||
Db 2187 AACCCCATCTCTACTAAAAATACAGAAATTAGCCGGGC 2224

RESULT 4
US-09-738-124-1

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Sequence 1Application US/09758124
Patent No. US20020006391A1

GENERAL INFORMATION:
APPLICANT: SMITH, Craig A.
APPLICANT: GOODMAN, Raymond G.
APPLICANT: BECKMANN, M. Patricia
TITLE OF INVENTION: TUMOR NECROSIS FACTOR-ALPHA AND -BETA RECEPTORS
FILE REFERENCE: A7895
CURRENT APPLICATION NUMBER: US/09/758,124
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 08/953,268
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 08/555,629
PRIOR FILING DATE: 1995-11-09
PRIOR APPLICATION NUMBER: 08/468,453
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/038,765
PRIOR FILING DATE: 1993-03-13
PRIOR APPLICATION NUMBER: 07/523,635
PRIOR FILING DATE: 1990-05-10
PRIOR APPLICATION NUMBER: 07/421,417
PRIOR FILING DATE: 1989-10-13
PRIOR APPLICATION NUMBER: 07/405,370
PRIOR FILING DATE: 1989-09-11
PRIOR APPLICATION NUMBER: 07/403,241
PRIOR FILING DATE: 1989-09-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 1641
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (88)..(1473)
NAME/KEY: mat_peptide
LOCATION: (154)..(1470)
NAME/KEY: sig_peptide
LOCATION: (88)..(153)
IS-09-758-124-1

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Query Match	17.3%	Score 453	DB 10	Length 1641
Best Local Similarity	96.98%	Pred. NO. 2e-87		
Matches 462	Conservative	0	Mismatches 15	Indels 0
			Gaps	0
QY	97	UACCCCAACCCATCTTGTGCTTAGCAGATTCCTCCCTGTGGCCATGGACCCAGATC	156	
DB	1165	GAGCGCCGGGCGAGCCGCGAGCTCAATATCTTCCCTCGTGGCCATGGACCCAGATC	1224	
QY	157	AATGTACCGTCATGTGTGAAGCTGTGTAGACGCTGTGACCCACACCTACAGTGTCTCTCC	216	
DB	1225	AATGTACCTGCACTGTGTGACGCTGTGTAGACGCTGTGACACACCTACAGTGTCTCTCC	1284	
QY	217	CAAGCCAGCTCCACATATGGGAGACACAGATTCACAGCCCTCGGAGTCCCGCAAGAGCAG	276	
DB	1285	CAAGCCAGCTCCACATATGGGAGACACAGATTCACAGCCCTCGGAGTCCCGCAAGAGCAG	1344	
QY	277	CAGGTCCCTCTTCCCAAGGAGGAATGTGCTTTGGGTACAGCTGTGAGAGCCACAGAGCC	336	
DB	1345	CAGGTCCCTCTTCCCAAGGAGGAATGTGCTTTGGGTACAGCTGTGAGAGCCACAGAGCC	1404	
QY	337	CTCTCTGGGAGACACGCAAGAGAAAGCCCGCCCTTTGGAGAGCTGTGATGCTGGGATGAAG	396	
DB	1405	CTCTCTGGGAGACACGCAAGAGAAAGCCCGCCCTTTGGAGAGCTGTGATGCTGGGATGAAG	1464	
QY	397	CCGCAATTAACCAAGGCGGCTGTGGGCTGTGCTGTAGCCCAAGGTGGGCTGTAGCCCTGACAG	456	
DB	1465	CCGCAATTAACCAAGGCGGCTGTGGGCTGTGCTGTAGCCCAAGGTGGGCTGTAGCCCTGACAG	1524	
QY	457	ATACACCTCGGAAGGGGCGCCCTGTGCTCTTCCACAGCCCGCCACACATAGACATCTTAGAGCTCT	516	
DB	1525	ATACACCTCGGAAGGGGCGCCCTGTGCTCTTCCACAGCCCGCCACACATAGACATCTTAGAGCTCT	1584	

Oy	517	TTCGGGACCAGTCTCCTAGTGCCCTCACAGCGGCAGCCTCCCTGTGACGTGCAG	573
Db	1585	TTCGGGACCAGTCTCCTAGTGCCCTCACAGCGGCAGCCTCCCTGTGACGTGCAG	1641
	RESULT 5		
	US-09-777-564-984/c		
	: Sequence 984, Application US/09777564		
	: Patent No. US20020022591A1		
	GENERAL INFORMATION:		
	: APPLICANT: Algate, Paul A.		
	: APPLICANT: Mannion, Jane		
	: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY		
	: TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER		
	: FILE REFERENCE: 210121.493		
	: CURRENT APPLICATION NUMBER: US/09/777,564		
	: CURRENT FILING DATE: 2001-02-05		
	: NUMBER OF SEQ ID NOS: 1730		
	: SOFTWARE: FastSeq for Window Version 4.0		
	: SEQ ID NO 984		
	: LENGTH: 336		
	: TYPE: DNA		
	: ORGANISM: Homo sapiens		
	US-09-777-564-984		

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Query Match      12.9%: Score 336: DB 10: Length 336:
Best Local Similarity 100.0%: Pred. No. 9.5e-63:
Matches 336: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1178 CCAAGTGTATCCCAAGTGGCCAGCTCTTGTGTGCGCTGTGTGTTTCGTCGTGTGGTGTG 1837
|||||
Db 336 CCAAGTGTATCCCAAGTGGCCAGCTCTTGTGTGCGCTGTGTGTTTCGTCGTGTGGTGTG 1837
QY 1838 GTAGCCCAAGGTGGTGAAGTGAATGGCCCTGTAACCCACTGAACCTGGAGTCTCTCC 1897
|||||
Db 276 GTAGCCCAAGGTGGTGAAGTGAATGGCCCTGTAACCCACTGAACCTGGAGTCTCTCC 217
QY 1898 CCAATTAGAGTCAGCCCTTCCCTCCAGGCGCAGGCGCCCTGCAGAGGGGAAACCACTGTGA 1957
|||||
Db 216 CCAATTAGAGTCAGCCCTTCCCTCCAGGCGCAGGCGCCCTGCAGAGGGGAAACCACTGTGA 157
QY 1958 GCCCTGGCCCGGATTTCTGGGAGGAGCAGGATGTAGAGGGGCTCCTGGAAAGGCTCACTCAG 2017
|||||
Db 156 GCCCTGGCCCGGATTTCTGGGAGGAGCAGGATGTAGAGGGGCTCCTGGAAAGGCTCACTCAG 97
QY 2018 GAGCATGGGAGTAAAGAGAAAGGCAATGAATTTGTATACAGAGCAGGGCCAGGGGTATTA 2077
|||||
Db 96 GAGCATGGGAGTAAAGAGAAAGGCAATGAATTTGTATACAGAGCAGGGCCAGGGGTATTA 37
QY 2078 ATTGTTGATTAATTCACCTGACCTTGACGCTTGGCAG 2113
|||||
Db 36 ATTGTTGATTAATTCACCTGACCTTGACGCTTGGCAG 1

RESULT 6
US-09-764-877-2146/c
: Sequence 2146, Application US/09764877
: Patent No. US20020147140A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
: FILE REFERENCE: PC005
: CURRENT APPLICATION NUMBER: US/09/764,877
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - refer to PALM or file wrapper
: NUMBER OF SEQ ID NOS: 4031
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2146
: LENGTH: 22609
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-764-877-2146

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Oy	1009	TCAGGCGAGGTGCAGTGGCTCACGCCCTATGATCCAGCACTTTGGAGGCTGAGCGGGT	1068
Dd	60334	TAAAGCCAGGTGGCGGGCTCACGCTGTAATCCAGAACTTTTGAGAGGCCAAGGTGGGGT	603933
Oy	1069	GGATCACCTGAGTGTGAGAGTTTCGAGACGACGCTGGCCAATGTTAAACCCTCATCTCT	1128
Dd	60394	GGATCACCTGAGGTCAGGACTTCAAGTCTAGGTGGTTCAAATGTGTGAACCCCATCTCT	604533
Oy	1129	ACTAAAATACAGAAATTAGCGGCGCGTGGGCGGCGGACCATTAAGCCAGCTACTTCAG	1188
Dd	60454	ACTAAAATACAAAAATTTTAGCCGGCGTGTGTGGCGGCGCTGTAAATCCAGCTACTTCAG	605133
Oy	1189	AAGCTGAGGCTGGGAAATCGTTTGAACCCGCGAAGCGGAGCTTGCAGGAGCCCGGATC	1248
Dd	60514	GAGGTTGAGGACGAGAANTCGCTTGACCTGGAGGCGGAGGTTGCAGTGAAGCCGAGATC	605733
Oy	1249	ACGGCACTGCAC TTCAGGCTGGGCGCAGAGCGAGAGTCTGTCTCAAAAGAAAAAAAAA	1308
Dd	60574	GCGCGCACTGCAC TCCGCTGGAGCAGACAGAGTAGAGACTCTGTCAAAAAAAAAAAAAA	606333
Oy	1309	AA 1310	
Dd	60634	AA 60635	

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RESULT 13
US-09-954-456-2116
: Sequence 2116 Application US/09954456
: Patent No. US20020115057A1
: GENERAL INFORMATION:
: APPLICANT: Young, Paul
: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer

```

```

1 CURRENT APPLICATION NUMBER: US/09/954,456
2
3 CURRENT FILING DATE: 2001-09-18
4
5 PRIOR APPLICATION NUMBER: US/60/233,617
6
7 PRIOR FILING DATE: 2000-09-18
8
9 PRIOR APPLICATION NUMBER: US/60/234,052
10
11 PRIOR FILING DATE: 2000-09-20
12
13 PRIOR APPLICATION NUMBER: US/60/234,923
14
15 PRIOR FILING DATE: 2000-09-25
16
17 PRIOR APPLICATION NUMBER: US/60/235,134
18
19 PRIOR FILING DATE: 2000-09-25
20
21 PRIOR APPLICATION NUMBER: US/60/235,637
22
23 PRIOR FILING DATE: 2000-09-26
24
25 PRIOR APPLICATION NUMBER: US/60/235,638
26
27 PRIOR FILING DATE: 2000-09-26
28
29 PRIOR APPLICATION NUMBER: US/60/235,711
30
31 PRIOR FILING DATE: 2000-09-27
32
33 PRIOR APPLICATION NUMBER: US/60/235,720
34
35 PRIOR FILING DATE: 2000-09-27
36
37 PRIOR APPLICATION NUMBER: US/60/235,840
38
39 PRIOR FILING DATE: 2000-09-27
40
41 PRIOR APPLICATION NUMBER: US/60/235,863
42
43 PRIOR FILING DATE: 2000-09-27
44
45 NUMBER OF SEQ ID NOS: 2276
46
47 SOFTWARE: PatentIn version 3.0
48
49 SEQ ID NO 2116
50
51 LENGTH: 145831
52
53 TYPE: DNA
54
55 ORGANISM: Homo sapiens
56
57 US-09-954-456-2116

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Query Match	9.1%;	Score 238;	DB 10;	Length 145831;
Best Local Similarity	86.8%;	Pred. No. 2.7e-41;		
Matches 262;	Conservative 0;	Mismatches 40;	Indels 0;	Gaps 0;

QY	1009	TTCAGCCAGGTGAGTGGCTCAACGCTATGATGACCCAGCATTTGGAGCTGAGACGGCGT	1068
Db	60334	TAAAGCCAGGTGCGGTGGCTCAACGCTTGTAATCCAGCAATTTGAGAGGCCCAAGGTGGGT	60393
Y	1069	GGATCACTTGAGTGTAGAGTTCGAGAGACAGCGTGGCCCAACATGCTAAACCCCATCTCT	1128

Db	60394	GGATACCTTAGGTCAGGAGTTCAAGTCAGTGTGTAACATGTATAAACCCTATCTC	604533
OY	1129	ACTAAATATACAGAAATTAGCCGGCGGTGTGGCGGACCTATATGTCCAGCTACTCAG	1188
Db	60454	ACTAAATATCAAAATTTTAGCCGGCGGTGTGGCGGCGCTGTAAATCCAGCTACTCAG	60513
OY	1189	AAGCCTGAGCCTGGGAATCTGTTGAACCCGGGAACGCGAGCTTGACAGGAGCGGAGATC	1248
Db	60514	GAGTTGAGCGACGAGATATCTGTTAACTGGGAGCGGAGAGTTGCAGTATAGCCGAGATC	60573
OY	1249	ACGCGATGAGATCCAGCCTGGGCGGACGACGAGAGATCTCTCTCAAAAGAAAAA	1308
Db	60574	CGCGCACTGCATCTGCTGCGAGCGACAGATGAGATCTCTCTCAAAAAAAAAA	60633
OY	1309	AA 1310	
Db	60634	AA 60635	

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RESULT 14
US-09-764-904-71/C
; Sequence 71, Application US/09764904
; Patent No. US20020173454A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA122
; CURRENT APPLICATION NUMBER: US/09/764, 904
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 31994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-904-71

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Query Match	Similarity	9.1%	Score 237.8	DB 9:	Length 31994:
Best Local	Similarity	85.0%	Pred. No. 21e-41:		
Matches 266:	Conservative	0:	Mismatches 47:	Indels	Gaps 0:
QY 998	AAAGATCAACCTCAGAGCCAGCGATGCTACAGTGGCTCACCCCTATGATATCCACAGACTTTGGAGG	1057			
DB 18379	AAAGAGGGGATACAGAGCCAGGGGTGGAGGCTCACACCTTTATCCAGACCTTTGGAGG	18320			
QY 1058	CTGAGCGGGGTGGATCACCTGAGGTTAGAGATTGAGACACAGCCCTGGCCACATGGTAA	1117			
DB 18319	CCAAAGGTGGGCGAGATCACTTTGAGTGCACAGATTGAGACACAGCTGGCCCAAGCTGGTAA	18260			
QY 1118	ACCCCATCTCTACTTAAAAATACAGAAATTAAGCGGGGCGCTGGTGGGGGAGCACTATATGTC	1177			
DB 18255	ACCCCGTCTCTTACCAAAATATACAAAAATTAATGCGGGCATGGTGGGGCGGCTATATATCC	18200			
QY 1178	CAGTACTACAGAGCCTGAGGCTGGGAAATCTGTTGAACCCCGGAAAGCGAGGATTGCAGG	1237			
DB 18199	GAGCTACTTGGGAGGCTGAGAGGAGAGATTCGCTTGAACCCAGAGAGCGAGAAGTTGCCACT	18140			
QY 1238	GAGCCGAGATCAGGCCACTGCACCTCAGGCTGGGCGAGAGAGCGAGAGTCTGTCAAAA	1297			
DB 18139	GAGCCGAGATCATGCGCACTGACCTCAGGCTGGGGGAGAGAGTAAGACCTCTGTCAAAA	18080			
QY 1298	GAIAAAAAAAAAA 1310				
DB 18079	AAAAAAAAAAAAA 18067				

RESULT 15
US-09-764-860-599/c
; Sequence 599, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 599
LENGTH: 31994
TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-860-599

Query Match 9.1%; Score 237.8; DB 10; Length 31994;
Best Local Similarity 85.0%; Pred. No. 2,1e-41;

Matches 266; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

OY 998 AAGCATCACCTCAGGCGGTGAGTGCAGTGGCTCAGCGCTATGATCCAGCATTGGGAGG 1057
||| | ||||| | ||||| ||| ||||| ||||| |||||
Db 18379 AAGAGGCGATTAACAGGCGCGGTGAGGCTCAGACCTGTATCCAGCATTGGGAGG 18320
OY 1058 CTGAGGCGGCGGTGAGTCACCTGAGGTTAGAGTTGAGACCAAGCTGGCCACATGATAA 1117
| ||| ||| ||||| ||||| | ||||| ||||| ||||| |||||
Db 18319 CCAAGGTGGGAGATCACTTGAGGTCACGAGTTGAGACCAAGCTGGCCACATGATAA 18260
OY 1118 ACCCCATCTCTACTAAATACAGAAATTAGCCGGGCGTGTGGCGGCGCCTATAGTCC 1177
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 18259 ACCCGTCTCTACCAAAATTAAGCCGGCATGTGGCGGCGCTATATATCC 18200
OY 1178 CAGCTACTCAGAAAGCTGAGGCTGGGAAATCGTTGAACCCGGGAAGCGAGTTGCAGG 1237
||||| | ||| || | ||||| || ||||| ||||| ||| ||||| |||||
Db 18199 CAGCTACTTGGGAGGCTGAAGCAGGAGATCGCTTGAACCCAGAGCGAGAGTTGCAGT 18140
OY 1238 GAGCCGAGATCACGCCACTGCACTCCAGCCTGGCGACAGAGAGAGTGTCTCAAAA 1297
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 18139 GAGCCGAGATCACTGCACTCCAGCCTGGCGACAGAGTAAGACTGTCTCAAAA 18080
OY 1298 CAAAAAATAAAA 1310
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 18079 AAAAAAATAAAA 18067

Search completed: December 5, 2002, 23:53:17
Job time: 1341.01 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 23:30:25 ; Search time 45.5918 Seconds
(without alignments)
14043.341 Million cell updates/sec

Title: US-09-856-937a-2

Perfect score: 22
Sequence: 1 gtagctgcaagatgaactcac 22

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Geneml:
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rod:*
36: em_hg_man:*
37: em_hg_vtl:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.8	85.5	103287	2	AC084034
2	18.8	85.5	194871	9	CNS01DRV
3	18.4	83.6	61823	2	AC108413
4	18.4	83.6	89604	9	AC108049
5	18.4	83.6	160505	2	AC112572
6	18.4	83.6	163363	2	AC123249
7	18.8	81.8	172475	9	AC025613
8	18.8	81.8	187282	9	AC019063
9	18.8	81.8	226233	9	AC067717
10	17.8	80.9	1143	6	AX278138
11	17.8	80.9	1218	6	AX278135
12	17.8	80.9	1413	9	AF169312
13	17.8	80.9	1855	6	AF079874
14	17.8	80.9	1860	9	AF153606
15	17.8	80.9	1862	6	AX079971
16	17.8	80.9	1869	6	AR194215
17	17.8	80.9	1869	6	AR194227
18	17.8	80.9	1869	6	AR207095
19	17.8	80.9	1869	6	AX201322
20	17.8	80.9	1869	6	AX464136
21	17.8	80.9	1873	6	E39784
22	17.8	80.9	1873	9	AB056477
23	17.8	80.9	1879	6	AX068560
24	17.8	80.9	1894	6	AX278133
25	17.8	80.9	1943	9	AF202636
26	17.8	80.9	8456	8	AB052794
27	17.8	80.9	8479	8	AB052792
28	17.8	80.9	11620	1	AE010665
29	17.8	80.9	45303	9	AC092300
30	17.8	80.9	57880	2	AC112401
31	17.8	80.9	66379	2	AC100415
32	17.8	80.9	87119	8	AC005897
33	17.8	80.9	94875	8	AC006429
34	17.8	80.9	106471	2	AC123178
35	17.8	80.9	127169	2	AC116683
36	17.8	80.9	140861	9	AC073349
37	17.8	80.9	151552	9	AL355863
38	17.8	80.9	169736	2	AC019305
39	17.8	80.9	171588	2	AC023198
40	17.8	80.9	171980	9	AL133701
41	17.8	80.9	172209	2	AC109117
42	17.8	80.9	181772	2	AC094169
43	17.8	80.9	184032	9	AC079226
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ALIGNMENTS

RESULT 1
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DEFINITION Homo sapiens chromosome 3 clone RP11-502H22, *** SEQUENCING IN
PROGRESS ***, 30 unordered pieces.
AC084034 AC084034.15 GI:20335777
AC084034 AC084034.15 GI:20335777
VERSION AC084034.15 GI:20335777
HTG: HTGS_PHASE1.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alshbrooks,S.L., Amaratunga,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbata, J., Benton, J., Blmage, K., Blankenburg, K., Bonnin, D.,
Bowle, S., Brileva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, U., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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Douthaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earmhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
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Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
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Honsl, F., Howard, S., Huber, J., Hulky, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
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Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Saverly, G.,
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Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Swalek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
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Wang, S., Ward, Moore, S., Warren, R., Washington, C., Watling, S.,
Williams, G., Williamson, A., Wleczky, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Welnstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 103287)
Worley, K.C.
Direct Submission
Submitted (11-OCT-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 103287)
Worley, K.C.
Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117994.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HCGG
Center clone name: RP11-502H22
----- Summary Statistics
Sequencing vector: M13:
Chemistry: Dye-terminator Big Dye: 63% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 117633 bases at least Q40
Consensus quality: 136061 bases at least Q30
Consensus quality: 148159 bases at least Q20
Estimated insert size: 141518: sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

FEATURES

source

1..103287
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"

(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
2194: contig of 2194 bp in length
2195
2294: gap of unknown length
2295
4434: contig of 2140 bp in length
4435
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4535
6710: contig of 2176 bp in length
6711
6810: gap of unknown length
6811
9027: contig of 2217 bp in length
9127: gap of unknown length
9128
11310: contig of 2183 bp in length
11311
11410: gap of unknown length
11411
13930: contig of 2520 bp in length
13931
14030: gap of unknown length
14031
16331: contig of 2501 bp in length
16332
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16332
19357: contig of 2726 bp in length
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22294: contig of 2837 bp in length
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22394: gap of unknown length
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24493: contig of 2099 bp in length
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24593: gap of unknown length
24594
27959: contig of 3266 bp in length
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64999: gap of unknown length
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70107: contig of 5108 bp in length
70108
70207: gap of unknown length
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AC108413 61823 bp DNA linear HTG 27-JAN-2002
LOCUS Mus musculus clone RP23-472M11, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC108413
AC108413.1 GI:18377223
VERSION HTG: HTGS_PHASE0.
KEYWORDS Mus musculus.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 61823)
Birken, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Unpublished
JOURNAL 2 (bases 1 to 61823)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barne, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,
Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B.,
Choepl, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Gilde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Lacombe, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McGowan, P., McKernan, K., Meldrum, J., Meneus, L., Michova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Rella, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Rovelli, M., Roy, A., Santos, R., Schauer, S., Schnupack, R., Seaman, S.,
Sever, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, K., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliou, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zemdek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (27-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE
JOURNAL
COMMENT
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L20284
Center clone name: 472_M_11

NOTE: This record contains 77 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 700: contig of 700 bp in length
701 800: gap of 100 bp
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3199 3909: contig of 711 bp in length
3910 4009: gap of 100 bp

4010 4707: contig of 698 bp in length
4708 4807: gap of 100 bp
4808 5430: contig of 683 bp in length
5491 5590: gap of 100 bp
5591 6308: contig of 718 bp in length
6309 6408: gap of 100 bp
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7113 7212: gap of 100 bp
7213 7910: contig of 698 bp in length
7911 8010: gap of 100 bp
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* 49927 50641: contig of 715 bp in length
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* 50742 51413: contig of 672 bp in length
* 51414 51513: gap of 100 bp
* 51514 52212: contig of 699 bp in length
* 52213 52312: gap of 100 bp
* 52313 53043: contig of 731 bp in length
* 53044 53143: gap of 100 bp
* 53144 53858: contig of 715 bp in length
* 53859 53958: gap of 100 bp
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* 54663 54762: gap of 100 bp
* 54763 55475: contig of 713 bp in length
* 55476 55575: gap of 100 bp

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Query Match 83.6% Score 18.4; DB 2; Length 61823;
 Best Local Similarity 95.0% Pred. No. 3.3e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TGATCTGCAAGTGAAGTCA 21
 DB 45566 TGATCTGCAAGTGAAGTCA 45585

RESULT 4 AC108049 89604 bp DNA linear PRI 23-MAR-2002
 LOCUS AC108049 Homo sapiens BAC clone RP11-325P16 from 2, complete sequence.
 ACCESSION AC108049
 VERSION AC108049.5 GI:19310337
 KEYWORDS HTG.
 SOURCE Homo sapiens.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 89604)
 AUTHORS Sulston, J.E. and Waterston, R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (1), 1097-1108 (1998)
 MEDLINE 99063792
 PUBMED 9847074
 REFERENCE 2 (bases 1 to 89604)
 AUTHORS Harris, A. and Cotton, M.
 TITLE The sequence of Homo sapiens BAC clone RP11-325P16
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 89604)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (24-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 89604)
 AUTHORS Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 89604)
 AUTHORS Waterston, R.
 TITLE Direct Submission
 JOURNAL Submitted (23-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 COMMENT On Mar 9, 2002 this sequence version replaced gi:18653771.

 Center: Washington University Genome Sequencing Center
 Web site: http://genome.wustl.edu/gsc
 Contact: saplens@wustl.wustl.edu

 Summary Statistics

 Center project name: H_NH0325P16

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
 The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the left is RP11-103L19, 2000 bp overlap; the clone sequenced to the right is RP11-19J8. Actual end of this clone is at base position 89604 of RP11-325P16.

Polymorphisms have been identified between AC016994, AC096663, and AC108049.

FEATURES Data from AC016994 was used to finish this clone, AC108049.

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/chromosome="2"
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953. .1276
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1299. .1464
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3681. .3820
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4473. .4926
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repeat_region 27792. .27815
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Query Match 83.6% Score 18.4; DB 9; Length 89604;
Best Local Similarity 95.0% Pred. No. 3,3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TGATCTGCAAGTCACTCA 21
|||||

Db 20611 TGATCTGCAAGTCACTCA 20630

RESULT 5
AC112572 160505 bp DNA linear HTG 14-JUL-2002
LOCUS Rattus norvegicus clone CH230-7M8, *** SEQUENCING IN PROGRESS ***
DEFINITION 73 unordered pieces.
ACCESSION AC112572
VERSION AC112572.2 GI:21731408
KEYWORDS HTG: HTGS PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 160505)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., All-ouman,F.R., Allen,C.,

Alsbrooks, S.L., Amaralunga, H.C., Are, J.R., Ayele, M., Banks, T.,
 Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonin, D.,
 Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
 Burch, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
 Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
 Douthaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
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 Falls, T., Ferraguto, D., Flagg, N., Ford, J.J., Foster, P., Frantz, P.,
 Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
 Gortell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
 Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
 Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,
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 Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
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 Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
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 Miner, G., Miner, Z., Mitchell, T., Monabadi, K., Morgan, M., Morris, S.,
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 Nguyen, N., Nickerson, E., Nwokenwo, S., Ogund, M., Okunnu, G.,
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 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G.,
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 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstock, G. and Gibbs, R.

Unpublished
 2 (bases 1 to 160505)

Worley, K.C.
 Direct Submission
 Submitted (22-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 160505)

Worley, K.C.
 Direct Submission
 Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jul 11, 2002 this sequence version replaced gi:18860158.

----- Genome Center -----
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information -----
 Center project name: KGBB
 Center clone name: CH230-7M8
 ----- Summary Statistics -----
 Sequencing vector: Plasmid
 Chemistry: Dye-terminator Big Dye 100% of reads
 Assembly program: Phrap version 0.990329
 Consensus quality: 85656 bases at least Q40
 Consensus quality: 89242 bases at least Q30
 Consensus quality: 91841 bases at least Q20

----- NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently

* consists of 73 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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2402	3565:	contig of 1164 bp in length
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4837	4936:	gap of unknown length
4937	6418:	contig of 1462 bp in length
6419	6518:	gap of unknown length
6519	8010:	contig of 1492 bp in length
8011	8110:	gap of unknown length
8111	9241:	contig of 1131 bp in length
9242	9341:	gap of unknown length
9342	11003:	contig of 1662 bp in length
11004	11103:	gap of unknown length
11104	12448:	contig of 1345 bp in length
12449	12548:	gap of unknown length
12549	13795:	contig of 1247 bp in length
13796	13895:	gap of unknown length
13896	15042:	contig of 1147 bp in length
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18586	20162:	contig of 1577 bp in length
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26809	27815:	contig of 1007 bp in length
27816	27915:	gap of unknown length
27916	29566:	contig of 1651 bp in length
29567	29666:	gap of unknown length
29667	30945:	contig of 1279 bp in length
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31046	32586:	contig of 1541 bp in length
32587	32686:	gap of unknown length
32687	33767:	contig of 1081 bp in length
33768	33867:	gap of unknown length
33868	35090:	contig of 1223 bp in length
35091	35190:	gap of unknown length
35191	36325:	contig of 1135 bp in length
36326	36425:	gap of unknown length
36426	37693:	contig of 1268 bp in length
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39752	39851:	gap of unknown length
39852	41554:	contig of 1703 bp in length
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44309	44380:	contig of 1072 bp in length
44381	44480:	gap of unknown length
44481	45849:	contig of 1369 bp in length
45850	45949:	gap of unknown length
45950	47477:	contig of 1528 bp in length
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* 47578 48807: contig of 1230 bp in length
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* 65812 65911: gap of unknown length
* 65912 68609: contig of 2698 bp in length
* 68610 68709: gap of unknown length
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* 75991 77716: contig of 1726 bp in length
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* 82179 82278: gap of unknown length
* 82279 85301: contig of 3023 bp in length
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* 85402 88054: contig of 2653 bp in length
* 88055 88154: gap of unknown length
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Query Match      83.6% Score 18.4: DB 2: Length 160505;
Best Local Similarity 95.0% Pred. No. 3.1e+02;
Matches 19: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 2 TGATCTGCAAGATGACTCA 21
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Db 102916 TGATCTTCAAGATGACTCA 102935

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RESULT 6
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LOCUS Rattus norvegicus clone CH230-244B19, *** SEQUENCING IN PROGRESS
DEFINITION
***, 44 unordered pieces.
AC123249
AC123249 2 GI:21671666
HTG: HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 163363)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsdorcks,S.L., Amaraltinge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brileva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.P., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
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Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

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David,L.M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
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Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,Y., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wlezyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G., and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 163363)
Worley,K.C.
Direct Submission
Submitted (29-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 163363)
Worley,K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 2, 2002 this sequence version replaced gi:21240087.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center Project name: GTPN
Center Clone name: CH230-244B19
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 126344 bases at least Q40
Consensus quality: 131142 bases at least Q30
Consensus quality: 134321 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 44 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 1503: contig of 1503 bp in length
1504 1603: gap of unknown length
1604 3030: contig of 1427 bp in length
3031 3130: gap of unknown length
3131 4392: contig of 1262 bp in length
4393 4492: gap of unknown length
4493 5852: contig of 1360 bp in length
5853 5952: gap of unknown length
5953 7095: contig of 1043 bp in length
7096 8586: gap of unknown length
8587 8686: gap of unknown length
8687 9990: contig of 1304 bp in length
9991 10090: gap of unknown length
10091 11764: contig of 1674 bp in length
11765 11864: gap of unknown length
11865 13429: contig of 1565 bp in length
13430 13529: gap of unknown length
13530 14810: contig of 1281 bp in length
14811 14910: gap of unknown length
14911 16558: contig of 1648 bp in length
16559 18315: gap of unknown length
18316 18415: gap of unknown length
18416 20154: contig of 1739 bp in length
20155 20254: gap of unknown length
20255 22329: contig of 2075 bp in length
22330 22430: gap of unknown length
22430 24344: contig of 1915 bp in length
24345 26087: gap of unknown length
26088 26187: gap of unknown length
26188 28711: contig of 2524 bp in length
28712 31094: gap of unknown length
31095 31194: gap of unknown length
31195 34176: contig of 2982 bp in length
34177 34276: gap of unknown length
34277 36318: contig of 2042 bp in length
36319 38416: gap of unknown length
38417 38516: gap of unknown length
38517 40712: contig of 2196 bp in length
40713 40812: gap of unknown length
40813 43142: contig of 2330 bp in length
43143 43242: gap of unknown length
43243 46103: contig of 2861 bp in length
46104 46203: gap of unknown length
46204 49350: contig of 3147 bp in length
49351 49450: gap of unknown length
49451 51585: contig of 2135 bp in length
51586 51685: gap of unknown length
51686 54333: contig of 2648 bp in length
54334 54433: gap of unknown length
54434 57387: contig of 2954 bp in length
57388 57487: gap of unknown length
57488 59609: contig of 2122 bp in length
59610 59709: gap of unknown length
59710 61392: contig of 1683 bp in length
61393 61492: gap of unknown length
61493 64948: contig of 3456 bp in length
64949 65048: gap of unknown length
65049 69695: contig of 4647 bp in length
69696 69795: gap of unknown length
69796 73662: contig of 3867 bp in length
73663 73762: gap of unknown length
73763 78216: contig of 4454 bp in length
78217 78316: gap of unknown length
78317 83265: contig of 4949 bp in length
83266 83365: gap of unknown length
83366 87982: contig of 4517 bp in length
87983 94335: gap of unknown length
94335: contig of 6353 bp in length

```

```

* 94336 94435: gap of unknown length
* 94436 101393: contig of 6558 bp in length
* 101394 101493: gap of unknown length
* 101494 108508: contig of 7015 bp in length
* 108509 108608: gap of unknown length
* 108609 116416: contig of 7808 bp in length
* 116417 116516: gap of unknown length
* 116517 121947: contig of 5431 bp in length
* 121948 122047: gap of unknown length
* 122048 136820: contig of 14773 bp in length
* 136821 149385: gap of unknown length
* 149386 149485: contig of 12465 bp in length
* 149486 163363: gap of unknown length
* 163363: contig of 13878 bp in length.

FEATURES
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    1. 163363
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"
    /clone="CH230-244B19"

BASE COUNT  50158 a 29064 c 29515 g 48662 t 5964 others

ORIGIN
GATCGCAAGATGACCTCAC 22
11111111111111111111
Db 4638 GATCGAAAGATGACCTCAC 4619

Query Match      83.6%; Score 18.4; DB 2; Length 163363;
Best Local Similarity 95.0%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GATCGCAAGATGACCTCAC 22
11111111111111111111
Db 4638 GATCGAAAGATGACCTCAC 4619

RESULT 7
AC025613 172475 bp DNA linear PRI 02-SEP-2000
DEFINITION Homo sapiens chromosome 3 clone RP11-514J23, complete sequence.
ACCESSION AC025613
VERSION AC025613.14 GI:9964950
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 172475)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D.,
Federpiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R.,
Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J.,
Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
Unpublished
JOURNAL 2 (bases 1 to 172475)
Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federpiel, N.,
Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R.,
Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J.,
Yu, S. and Davis, R.W.
Direct Submission
TITLE Submitted (12-MAR-2000) DNA Sequencing and Technology Center,
JOURNAL Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
REFERENCE 3 (bases 1 to 172475)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D.,
Federpiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R.,
Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J.,
Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
Direct Submission
TITLE Submitted (02-SEP-2000) DNA Sequencing and Technology Center,
JOURNAL Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT On Sep 2, 2000 this sequence version replaced gi:8671904.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center
Center code: SDSRDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu

```


sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality/info/genbank.annotation.html>.

QUALSTAT-REPORT.

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source	1..226233 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3"
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repeat_region	813..1003 /rpt_family="L2"
repeat_region	1880..2018 /rpt_family="L1PA5"
STS	1880..2018 /standard_name="150150"
repeat_region	2315..2343 /rpt_family="AT_r1ch"
repeat_region	2464..2495 /rpt_family="L1PA5"
repeat_region	2700..2724 /rpt_family="(TC)n"
repeat_region	2726..2833 /rpt_family="(TC)n"
repeat_region	complement(2848..3157) /rpt_family="AluX"
repeat_region	3823..3846 /rpt_family="AT_r1ch"
repeat_region	4725..4970 /rpt_family="MIR"
repeat_region	complement(5370..5539) /rpt_family="L1M4"
repeat_region	complement(5755..5904) /rpt_family="AluY"
repeat_region	7691..7713 /rpt_family="AT_r1ch"
repeat_region	complement(7714..8516) /rpt_family="L1PA16"
repeat_region	complement(8675..8971) /rpt_family="AluX"
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repeat_region	10456..10478 /rpt_family="(TA)n"
repeat_region	complement(10749..11047) /rpt_family="AluSg"
repeat_region	12841..13103 /rpt_family="L1ME"
STS	13380..13658 /standard_name="183639"
repeat_region	complement(14885..15450) /rpt_family="MER68"
repeat_region	15802..15940 /rpt_family="MIR"
repeat_region	complement(16272..16626) /rpt_family="MLT2A"
repeat_region	17272..17407 /rpt_family="MLT1E1"
repeat_region	17468..17664 /rpt_family="MLT1E1"
repeat_region	complement(17856..18136) /rpt_family="MLT1J1"
repeat_region	complement(18170..18229) /rpt_family="MIR"
repeat_region	complement(18532..18623) /rpt_family="MIR"
repeat_region	complement(19880..19977) /rpt_family="MLT1E2"
repeat_region	19995..20499 /rpt_family="MER75"
repeat_region	complement(20503..20909) /rpt_family="MLT1D"
repeat_region	complement(23244..23404) /rpt_family="MIR"
repeat_region	23687..23709 /rpt_family="AT_r1ch"
repeat_region	23882..23945 /rpt_family="(TA)n"

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Best Local Similarity 100.0%; Score 18; DB 9; Length 226233;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ATCTGCAAGATGAACCTCA 21
|||||
Db 87623 ATCTGCAAGATGAACCTCA 87606

RESULT 10	LOCUS	SEQUENCE	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL
AX278138	AX278138	Sequence 6 from Patent WO0177151.	AX278138	AX278138	AX278138.1	GI:16605208	human.	Homo sapiens	1	Holtzman,D.A., Spiegelman,B.M. and Yoon,C.H.	Farg proteins and nucleic acid molecules and uses therefor
										Patent: WO 0177151-A 6 18-OCT-2001;	Millennium Pharmaceuticals, Inc. (US) ; DANA-FARBER CANCER INSTITUTE, INC. (US)

FEATURES	Location/Qualifiers
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SDGQWTVIQRHDSVDFNRPWEAYKAGFGDPHGEFNLGLEKVSHTGDRNSRLAOL
LRDMGNAELLOFVHLDGEDTAYSLQTAAPVAGOLGATTVPPSGLSVPESTMDODHL
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TMLIQPMAAEAAS"
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BASE COUNT 278 a 463 c 444 g 228 t

ORIGIN

Query Match 80.9% Score 17.8; DB 9; Length 1413;
Best Local Similarity 90.5%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCA 21
|||||
Db 790 GTGACTGCAAGATGACTCA 724

RESULT 14
AX079874 1855 bp DNA Linear PAT 22-FEB-2001
LOCUS Sequence 5 from Patent WO0105971.
DEFINITION AX079874
ACCESSION AX079874
VERSION AX079874.1 GI:13159399
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1855)
REFERENCE Shimkets, R.A. and Fernandes, E.
TITLE Secreted polypeptides and corresponding polynucleotides
JOURNAL Patent: WO 0105971-A 5 25-JAN-2001;
Curagen Corporation (US)
FEATURES
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AF153606
AF153606.1 GI:5231136
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1860)
REFERENCE Kim, M.K., Kim, Y.H., Seo, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,
Hwang, S.Y., Im, S.U., Jung, E.J., Lee, J.H. and Kim, J.C.
TITLE A catalogue of genes in the human dermal papilla cells as
identified by expressed sequence tags
JOURNAL Unpublished
2 (bases 1 to 1860)
AUTHORS Kim, M.K., Kim, Y.H., Suh, J.M., Lee, H.M., Chung, H.J., Sohn, M.Y.,
Hwang, S.Y., Im, S.U., Jung, E.J. and Kim, J.C.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-1999) Immunology, Kyungpook National University,
School of Medicine, 101 Dongin Dong, Jung Gu, Taegu, Taegu 700-422,
South Korea
FEATURES
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154..1371
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/protein_id="A041088.1"
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AHGLDLOCGCANTGAPPOSARAGARISACGACGCTEGSTDLPLAPSRVPEVL
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LRDKNCASLSGGMWFGTCSHNLNGOYFRSIPQQRKLLKGIKMTWGRYYPLOAT
TMLIQPMAAEAAS"

BASE COUNT 391 a 584 c 573 g 312 t

ORIGIN

Query Match 80.9% Score 17.8; DB 9; Length 1860;
Best Local Similarity 90.5%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCA 21
|||||
Db 790 GTGACTGCAAGATGACTCA 810

Search completed: December 6, 2002, 03:54:50
Job time : 457.792 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 16:34:38 ; Search time 5.2698 Seconds

(without alignments)
9365.950 Million cell updates/sec

Title: US-09-856-937a-2

Perfect score: 22

Sequence: 1 gtagatcgcaagaatgaactac 22

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	AAA49208	Human tumour necro
2	22	100.0	22	AAA48202	Forward PCR primer
3	18.8	85.5	22	AAK68202	Human immune/haema
4	18.8	85.5	22	AAK61760	Human immune/haema
5	17.8	80.9	305	AAO39672	Expressed Sequence
6	17.8	80.9	305	AAO39084	Human brain Expres
7	17.8	80.9	432	ABA08330	Human hepatic angl
8	17.8	80.9	448	AAS88089	DNA encoding novel
9	17.8	80.9	474	AAS88094	DNA encoding novel

10	17.8	80.9	651	24	AAO22561	Human FDRG (fibrin
11	17.8	80.9	1143	24	AAO22560	Human mature FDRG
12	17.8	80.9	1218	24	AAO22559	Human FDRG (fibrin
13	17.8	80.9	1221	21	AAZ97139	Human gene 75 DNA
14	17.8	80.9	1379	21	AAZ97132	Human secreted pro
15	17.8	80.9	1413	24	ABO88100	Human secreted pro
16	17.8	80.9	1484	23	AAS88098	Human osteoblast d
17	17.8	80.9	1827	21	AAC69692	DNA encoding novel
18	17.8	80.9	1855	22	AAE30190	Novel Human protei
19	17.8	80.9	1858	20	AAK85599	Clone 11696905-0-4
20	17.8	80.9	1860	24	ABO88099	DNA encoding a hum
21	17.8	80.9	1862	22	AAO25606	Human osteoblast d
22	17.8	80.9	1865	20	AAK33970	Human angiotensin
23	17.8	80.9	1869	21	AAK33970	Human TIE ligand N
24	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
25	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
26	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
27	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
28	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
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31	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
32	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
33	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
34	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
35	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
36	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
37	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
38	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
39	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
40	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
41	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
42	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
43	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
44	17.8	80.9	1869	22	AAK33970	Human TIE ligand N
45	17.8	80.9	1869	22	AAK33970	Human TIE ligand N

ALIGNMENTS

RESULT 1
AAA49208
ID AAA49208 standard; DNA: 22 bp.
AC AAA49208:
DT 22-NOV-2000 (first entry)
XX
DE Human tumour necrosis factor alpha receptor 2 gene PCR primer TNFR2-CAF.
XX
KW Human: tumour necrosis factor alpha receptor 2; TNFR2; polymorphism;
KW osteoporosis; PCR primer: ss.
XX
OS Homo sapiens.
XX
PN WO200032826-A1.
XX
PD 08-JUN-2000.
XX
PF 30-NOV-1999: 99MO-US28403.
XX
PR 30-NOV-1998: 98US-0110268.
XX
PA (UYDR-) UNIV DREXEL.
XX
PI Spot11a LD:
XX
DR WPI: 2000-412362/35.
XX
PT Identifying individuals at risk of developing osteoporosis comprises
PT assessing the genotype of a tumor necrosis factor-alpha 2 receptor gene
PT in a DNA sample from an individual -

XX Example 2; Page 11; 21pp; English.

PS The present sequence is a PCR primer for the (CA)₁₆ repeat of intron 4 of

CC the human tumour necrosis factor alpha receptor 2 (TNFR2) gene. It was

CC thought that this intron might contain a polymorphism related to

CC osteoporosis. However, it was shown that this was not so. However, exon

CC 10 contains three polymorphic sites. By determining the genotype of an

CC individual it is possible to identify those at risk of osteoporosis,

CC which is characterized by low bone density and fragile bones, later in

CC life. Those at greatest risk are those who possess allele 1, which is the

CC rarest allele. This is particularly useful as many cases of osteoporosis

CC go undetected at present.

XX

SQ Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.5; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCAG 22

DB 1 GTGATCTGCAAGATGACTCAG 22

RESULT 2

AAA8202 ID AAA8202 standard; DNA: 22 BP.

XX AAA8202:

AC 15-SEP-2000 (first entry)

DT

DE Forward PCR primer for detection of TNFRSF1B intron 4 polymorphism.

XX

XX Tumour necrosis factor: TNF; TNFR2; TNFRSF1B; PCR primer:

KM tumour necrosis factor receptor superfamily member 1b; human;

KM cardiovascular disease; coronary artery disease;

KM non-insulin dependent diabetes mellitus; neuropathy in NIDDM;

KM essential hypertension; hyperlipidemia; diabetic neuropathy;

KM vasoprotective; antihypertensive; lipid-lowering;

KM chromosome 1p36.2; DIS2834; ss.

XX

OS Homo sapiens.

XX

XX WO200031293-A1.

PN 02-JUN-2000.

PD

XX 25-NOV-1999; 99WO-AU01050.

PF

XX 25-NOV-1998; 98AU-0007323.

PR

XX (UNSY) UNIV SYDNEY.

PA

XX

PI Morris BJ:

XX

DR WPI: 2000-400096/34.

XX

XX

PT Method for diagnosing a predisposition to a complex polygenic disease

PT e.g. coronary heart disease, hyperlipidemia and non-insulin-dependent

PT diabetes mellitus comprises assaying chromosome 1 for a genetic marker

PT

XX

XX Claim 30; Page 3; 50pp; English.

XX

XX A novel method for determining a predisposition in a subject to a

CC complex polygenic disease involves assaying chromosome 1 for a

CC genetic marker indicative of a predisposition to the disease. This

CC method may be used for determining predisposition to cardiovascular

CC disease, coronary artery disease, non-insulin dependent diabetes

CC mellitus, neuropathy in NIDDM, essential hypertension, hyperlipidemia

CC and diabetic neuropathy. The method can be used for testing an

CC individual with a family history or in the early stages of a complex

CC polygenic disease to ascertain the chance of developing hypertension,

CC neuropathy or lipid disturbances such as high total cholesterol, high

CC low density lipoprotein cholesterol, abnormal apolipoprotein AI and

CC abnormal glycosylated haemoglobin. Once a complex polygenic disease

CC disposition has been identified the subject can be treated to prevent

CC or reduce the disease or delay its onset. The genetic marker used

CC in the method is DIS2834 and includes a CA repeat region in intron

CC 4 of the tumour necrosis factor receptor superfamily member 1b

CC (TNFRSF1B) gene. The marker is located at chromosome 1p36.2. The

CC present sequence is the forward PCR primer used for detection of

CC the TNFRSF1B intron 4 polymorphism.

XX

SQ Sequence 22 BP; 7 A; 5 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 22; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.5; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCAG 22

DB 1 GTGATCTGCAAGATGACTCAG 22

RESULT 3

AAK68202/C ID AAK68202 standard; DNA: 56743 BP.

XX AAK68202:

AC 06-NOV-2001 (first entry)

DT

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23014.

XX

XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;

KM cytostatic; gene therapy; vaccine; metastasis; ds.

XX

XX Homo sapiens.

PN WO200157182-A2.

XX

PD 09-AUG-2001.

XX

XX 17-JAN-2001; 2001WO-US01354.

PF

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209457.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 26-JUL-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0225868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0226924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0232406.
 PR 14-SEP-2000; 2000US-0232406.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0244617.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.

PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0146613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249285.
 PR 17-NOV-2000; 2000US-0249287.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM:
 XX
 DR WPI: 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure; SEQ ID NO 23014; 3071pp + Sequence Listing: English.
 XX
 CC AA54951 to AA64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AA62170 to AA69121. (I) Have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AA64703
 CC to AA67694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AA54942 to AA64950 and AA62169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 56743 BP: 14298 A; 13270 C; 14240 G; 14935 T; 0 other:
 Query Match 85.5%; Score 18.8; DB 22; Length 56743;
 Best Local Similarity 90.9%; Pred. No. 56;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GTGATCTGCACAGTGAATCTCAC 22

Db 16373 GTGAACTGCAAGAGAACTCAG 16352
|||||
RESULT 4
ID AAK81760 standard; DNA: 56743 BP.
XX
AC AAK81760;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:36572.
XX
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KM cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001: 2001WO-US01354.
XX
PR 31-JAN-2000: 2000US-0179065.
PR 04-FEB-2000: 2000US-0180628.
PR 24-FEB-2000: 2000US-0184664.
PR 02-MAR-2000: 2000US-0186350.
PR 16-MAR-2000: 2000US-0189874.
PR 17-MAR-2000: 2000US-0190076.
PR 18-APR-2000: 2000US-0198123.
PR 19-MAY-2000: 2000US-0205515.
PR 07-JUN-2000: 2000US-0209467.
PR 28-JUN-2000: 2000US-0214886.
PR 30-JUN-2000: 2000US-0215135.
PR 07-JUL-2000: 2000US-0216647.
PR 07-JUL-2000: 2000US-0216880.
PR 11-JUL-2000: 2000US-0217487.
PR 11-JUL-2000: 2000US-0217496.
PR 14-JUL-2000: 2000US-0218290.
PR 26-JUL-2000: 2000US-0220963.
PR 26-JUL-2000: 2000US-0220964.
PR 14-AUG-2000: 2000US-0224518.
PR 14-AUG-2000: 2000US-0224519.
PR 14-AUG-2000: 2000US-0225213.
PR 14-AUG-2000: 2000US-0225266.
PR 14-AUG-2000: 2000US-0225267.
PR 14-AUG-2000: 2000US-0225268.
PR 14-AUG-2000: 2000US-0225270.
PR 14-AUG-2000: 2000US-0225447.
PR 14-AUG-2000: 2000US-0225757.
PR 14-AUG-2000: 2000US-0225758.
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PR 22-AUG-2000: 2000US-0226681.
PR 22-AUG-2000: 2000US-0226868.
PR 23-AUG-2000: 2000US-0227182.
PR 30-AUG-2000: 2000US-0228924.
PR 01-SEP-2000: 2000US-0229287.
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PR 08-SEP-2000: 2000US-0231244.
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PR 08-SEP-2000: 2000US-0231414.
PR 08-SEP-2000: 2000US-0232080.
PR 08-SEP-2000: 2000US-0232081.
PR 12-SEP-2000: 2000US-0231968.
PR 14-SEP-2000: 2000US-0232397.
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PR 14-SEP-2000: 2000US-0232399.
PR 14-SEP-2000: 2000US-0232400.
PR 14-SEP-2000: 2000US-0232401.
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PR 14-SEP-2000: 2000US-0233063.
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PR 21-SEP-2000: 2000US-0234223.
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PR 26-SEP-2000: 2000US-0235484.
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PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
PR 02-OCT-2000: 2000US-0237040.
PR 13-OCT-2000: 2000US-0239935.
PR 13-OCT-2000: 2000US-0239937.
PR 20-OCT-2000: 2000US-0240960.
PR 20-OCT-2000: 2000US-0241221.
PR 20-OCT-2000: 2000US-0241785.
PR 20-OCT-2000: 2000US-0241786.
PR 20-OCT-2000: 2000US-0241787.
PR 20-OCT-2000: 2000US-0241808.
PR 20-OCT-2000: 2000US-0241809.
PR 20-OCT-2000: 2000US-0241826.
PR 01-NOV-2000: 2000US-0244617.
PR 08-NOV-2000: 2000US-0246474.
PR 08-NOV-2000: 2000US-0246475.
PR 08-NOV-2000: 2000US-0246476.
PR 08-NOV-2000: 2000US-0246477.
PR 08-NOV-2000: 2000US-0246478.
PR 08-NOV-2000: 2000US-0246523.
PR 08-NOV-2000: 2000US-0246524.
PR 08-NOV-2000: 2000US-0246525.
PR 08-NOV-2000: 2000US-0246526.
PR 08-NOV-2000: 2000US-0246527.
PR 08-NOV-2000: 2000US-0246528.
PR 08-NOV-2000: 2000US-0246532.
PR 08-NOV-2000: 2000US-0246609.
PR 08-NOV-2000: 2000US-0246610.
PR 08-NOV-2000: 2000US-0246611.
PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
PR 17-NOV-2000: 2000US-0249209.
PR 17-NOV-2000: 2000US-0249210.
PR 17-NOV-2000: 2000US-0249211.
PR 17-NOV-2000: 2000US-0249212.
PR 17-NOV-2000: 2000US-0249213.
PR 17-NOV-2000: 2000US-0249214.
PR 17-NOV-2000: 2000US-0249215.
PR 17-NOV-2000: 2000US-0249216.
PR 17-NOV-2000: 2000US-0249217.
PR 17-NOV-2000: 2000US-0249218.
PR 17-NOV-2000: 2000US-0249244.
PR 17-NOV-2000: 2000US-0249245.
PR 17-NOV-2000: 2000US-0249264.
PR 17-NOV-2000: 2000US-0249265.
PR 17-NOV-2000: 2000US-0249297.

PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI: 2001-483426/52.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis.

PS Disclosure: SEQ ID NO 36572; 3071pp + Sequence Listing; English.

CC AA05951 to AA064702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AA082170 to AA091921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AA064703
 CC to AA087694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AA05942 to AA054950 and AA082169
 CC represent sequences used in the exemplification of the present invention.

XX Sequence 56743 BP; 14298 A; 13270 C; 14240 G; 14935 T; 0 other;

Query Match 85.5%; Score 18.8; DB 22; Length 56743;

Best Local Similarity 90.9%; Pred. No. 56;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GTGATCTGCAAGATGACTCAC 22

DB 16373 GTGAAGCTGCAAGAACTCTCAC 16352

RESULT 5

AA039672 ID AA039672 standard; DNA: 305 BP.

AC AA039672;

DT 20-MAY-1993 (first entry)

DE Expressed Sequence Tag human gene marker EST00364.

KM expressed sequence tag: human genome project: chromosome;

KW human gene sequencing; PCR mapping; somatic cell hybrids;

XX sublocalisation; gene tagging; tissue typing.

OS Synthetic.

PN WO9300353-A.
 XX 07-JAN-1993.
 PD 19-JUN-1992; 92WO-US05222.
 XX 20-JUN-1991; 91US-0716831.
 PR 12-FEB-1992; 92US-0837195.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PA Adams MD, Venter JC;
 PI WPI: 1993-036325/04.
 DR Particular expressed sequence tags from human CDNA - corresponds
 PT to transcription prods. of genes, useful for tagging genes,
 PT mapping chromosomes and tissue typing
 XX Claim 3; Page 96; 199pp; English.
 CC This sequence represents an EST (expressed sequence tag) ESTs are
 CC markers for human genes actually transcribed in vivo. Unlike the random
 CC genomic DNA sequence tagged sites (STSs), ESTs point directly to
 CC expressed genes. The use of ESTs could facilitate the tagging of most
 CC expressed human genes within a few years at a fraction of the cost of
 CC complete genomic sequencing. Using PCR primers AA039419-039580 (sequences
 CC designed from the ESTs) sublocalisation of an EST can be achieved with
 CC panels of fragments from specific chromosomes or pools of large genomic
 CC clones in an analogous manner. This sequence represents EST00364.
 XX
 SQ Sequence 305 BP; 65 A; 69 C; 110 G; 59 T; 2 other;
 Query Match 80.9%; Score 17.8; DB 14; Length 305;
 Best Local Similarity 90.5%; Pred. No. 74;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GTGATCTGCAAGATGACTCA 21
 DB 83 GTGAAGCTGCAAGAACTCTCA 103
 RESULT 6
 ID AA059084 standard; CDNA: 305 BP.
 AC AA059084;
 XX 16-MAR-1994 (first entry)
 DE Human brain Expressed Sequence Tag EST00364.
 XX Gene transcription product; genetic markers; tagging; in vivo;
 KM transcription; mapping; locations; chromosomes; chromosomal; ss.
 XX Homo sapiens.
 OS WO9316178-A.
 PN 19-AUG-1993.
 PD 12-FEB-1993; 93WO-US01294.
 XX 12-FEB-1992; 92US-0837195.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PA Adams MD, Moreno RF, Venter CJ;
 PI WPI: 1993-272882/34.
 DR Enriched oligonucleotides and corresp. sequences - used as
 PT markers for human genes transcribed in-vivo, facilitate tagging

PT of most human genes
XX
PS Example 1: Page 118; 500pp; English.
XX
CC The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for mapping locations of expressed genes
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prep. of antisense sequences, probes and constructs.
CC EST00364 has a "marginal" coding probability as evaluated using the
CC coding-region prediction program CMM.
CC See also AA059041-061440.
XX
SO Sequence 305 BP; 63 A; 70 C; 109 G; 59 T; 4 other;

Query Match 80.9%; Score 17.8; DB 14; Length 305;
Best Local Similarity 90.5%; Pred. No. 74;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGACTCA 21
DB 83 GTGAACTCGACAGTGAACCTCA 103

RESULT 7
ABA08330
ID ABA08330 standard; cDNA: 432 BP.
XX
AC ABA08330;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human hepatic angiotensin-related protein homologue cDNA, SEQ ID NO:106.
XX
KW Human: cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; actlyin;
KW Inhibin; chemotaxis; chemokinesis; tumour; haematopoietic disorder;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
KW antifungal; veterinary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dirmanac RT;
XX
DR WPI: 2001-457740/49.
DR P-PSDB: ABB11086.
XX
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
XX
PS Claim 1; Page 378; 1963pp; English.

XX
CC Sequences ABB10961-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities, stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention.
XX
SO Sequence 432 BP; 94 A; 119 C; 125 G; 94 T; 0 other;

Query Match 80.9%; Score 17.8; DB 22; Length 432;
Best Local Similarity 90.5%; Pred. No. 78;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTGATCTGCAAGATGACTCA 21
DB 321 GTGAACTCGACAGTGAACCTCA 341

RESULT 8
AAS88089/C
ID AAS88089 standard; cDNA: 448 BP.
XX
AC AAS88089;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23893.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PR 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.